MycoKeys

MycoKeys 130: 1–49 (2026)
DOI: 10.3897/mycokeys.130.181430

Research Article

Taxonomy and phylogeny of saprobic Sordariomycetes (Ascomycota) from woody litter in terrestrial ecosystems of Yunnan Province, China

Guang-Cong Ren[1], Dhanushka Wanasinghe[2,3,4], Heng Gui[2,3], Zu-Yi Zhou[1], Xian Shi[1], Turki Kh. Faraj[4], Kai-Xuan Dong[1]

1 *School of Pharmacy, Guiyang Kangyang University, Guiyang 550081, China*
2 *Department of Economic Plants and Biotechnology, Yunnan Key Laboratory for Wild Plant Resources, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China*
3 *Center for Mountain Futures, Kunming Institute of Botany, Chinese Academy of Sciences, Honghe 654400, China*
4 *Department of Soil Science, College of Food and Agriculture Sciences, King Saud University, P.O. Box 145111, Riyadh 11362, Saudi Arabia*
Corresponding author: Dhanushka Wanasinghe (dnadeeshan@gmail.com)

Abstract

As part of our investigation into the diversity of woody litter fungi in Yunnan Province, China, we identified ten microfungal taxa associated with dead woody litter in terrestrial habitats. Based on detailed morphological comparisons and multigene phylogenetic analyses using Maximum Likelihood and Bayesian Inference, including non-translated loci and protein-coding regions, we identified three taxa as new species and seven collections as new records within Sordariomycetes. Three novel species are *Barrmaelia nixiensis*, *Biscogniauxia xishuangbannaensis*, *Neolinocarpon lincangense*, while *Jattaea algeriensis*, *Lasiosphaeris hispida*, *Neoleptosporella camporesiana*, *Planisphaeria karsti*, *P. reniformispora*, *Phaeoacremonium camporesii* and *Thyridium tiliae* represent new host records. Comprehensive morphological descriptions and illustrations are provided to support the identification and classification of these taxa.

Key words: 3 new species, 7 new records, Barrmaeliaceae, Diaporthomycetidae, Graphostromataceae, Lasiosphaeridaceae, Linocarpaceae, Neoleptosporellaceae, Sordariomycetidae

OPEN ACCESS

Academic editor:
Sajeewa Maharachchikumbura
Received: 5 December 2025
Accepted: 3 February 2026
Published: 18 March 2026

Citation: Ren G-C, Wanasinghe D, Gui H, Zhou Z-Y, Shi X, Faraj TKh, Dong K-X (2026) Taxonomy and phylogeny of saprobic Sordariomycetes (Ascomycota) from woody litter in terrestrial ecosystems of Yunnan Province, China. MycoKeys 130: 1-49. https://doi.org/10.3897/mycokeys.130.181430

Copyright: © Guang-Cong Ren et al.
This is an open access article distributed under terms of the Creative Commons Attribution License (Attribution 4.0 International – CC BY 4.0).

Introduction

Woody litter is vital in forests, playing a key role in nutrient cycling and ecosystem balance (Bucher et al. 2004; Monkai et al. 2013; Marcot 2017). Fungi on the wood such as lignicolous fungi break down these woody litter, releasing essential nutrients into the environment (Boddy 2001; Bucher et al. 2004; Bebber et al. 2006; Lustenhouwer et al. 2020). Fungi also form beneficial partnerships with plants, like mycorrhizal associations, enhancing nutrient absorption and promoting plant growth (Fukasawa et al. 2011; Fukasawa 2021; Delavaux et al. 2023). They produce antimicrobial compounds, aiding in pathogen suppression (Lonsdale et al. 2008; Hyde et al. 2019; Sułkowska-Ziaja et al. 2023). Despite their crucial ecological roles, fungal diversity and interactions with host

associations remain poorly understood. Therefore, there is a growing interest in exploring various ecosystems to uncover unidentified fungal species and better understand their ecological roles (Wanasinghe et al. 2024, 2025).

Sordariomycetes is a highly diverse class of fungi within the phylum Ascomycota, playing crucial roles across various ecosystems (Huang et al. 2021). They serve as valuable biocontrol agents in agriculture and contribute significantly to pharmaceutical and biotechnological industries through the production of bioactive secondary metabolites (Hyde et al. 2019, 2024a; Chen et al. 2023). The majority of sordariomycetous species are characterized by perithecial ascomata and inoperculate unitunicate asci, while their asexual morphs are primarily hyphomycetous or coelomycetous (Maharachchikumbura et al. 2016; Samarakoon et al. 2022). This class includes seven subclasses, 56 orders, 215 families, and 1,924 genera (including 390 genera of uncertain placement) (Hyde et al. 2024b), exhibiting higher taxonomic diversity. Sordariomycetes occupy a wide range of ecological niches, live as pathogens, endophytes, saprobes, epiphytes, coprophilous organisms, fungicolous fungi, mycoparasites, lichenized or lichenicolous species (Maharachchikumbura et al. 2015, 2016; Samaradiwakara et al. 2023). They thrive in both aquatic (freshwater and marine) and terrestrial habitats, with terrestrial environments being the most common (Maharachchikumbura et al. 2015; Chen et al. 2023). This global distribution underscores the adaptability and ecological versatility of Sordariomycetes, making them integral components of diverse ecosystems.

Although Sordariomycetes were traditionally classified using morphology (ascomata, asci, ascospores and asexual morph traits) (Gautam et al. 2022), morphology alone is often constrained by plasticity, character overlap, and convergent evolution and asexual morphs are frequently absent or inconsistent (Samaradiwakara et al. 2023; Ekanayaka et al. 2025). Consequently, multi-locus phylogenetic data have become essential for accurate delimitation and evolutionary inference (Luo et al. 2019; Hyde et al. 2020b; Huang et al. 2021; Wang et al. 2024). Phylogenetic investigations based on multilocus DNA sequence data have shed light on the complex relationships among various taxa within the class (Samarakoon et al. 2023; Hyde et al. 2024b), facilitating major taxonomic revisions and the discovery of previously unrecognized lineages (Samarakoon et al. 2022, 2023; Bao et al. 2023; Yang et al. 2023). Given the paucity of distinctive morphological traits in several genera, such molecular-based analyses have become indispensable for accurate taxonomic placement.

Yunnan Province, with its complex topography, diverse climates, and rich vegetation, is a hotspot for fungal diversity (Feng and Yang 2018). Taxonomic studies of ascomycetes in the region have intensified in recent years, yielding over 300 novel species in the past five years alone (Phookamsak et al. 2024). We have conducted extensive field surveys over the past seven years, targeting lignicolous Ascomycota from woody litter (Ren et al. 2022a, 2022b, 2024). This study aims to document previously unaccounted sordariomycetous taxa from our collections, integrating morphological characteristics with multigene phylogenetic analyses. As a result, we introduce three novel species viz. *Barrmaelia nixiensis*, *Biscogniauxia xishuangbannaensis*, *Neolinocarpon lincangense*, and alongside seven new records for the region: *Jattaea algeriensis*, *Lasiosphaeris hispida*, *Neoleptosporella camporesiana*, *Planisphaeria karsti*, *P. reniformispora*, *Phaeoacremonium camporesii* and *Thyridium tiliae*.

Materials and methods

Sample collection, observation and isolation

Decayed woody samples were collected from mixed forest areas in China (Yunnan Province), in July 2019 and from July to December 2020, and brought to the laboratory in separate zip-lock plastic bags. Specimens were examined using a stereomicroscope (Olympus SZ61, Tokyo, Japan). Micro-morphological characteristics (i.e. ascomata, peridium, paraphyses, asci and ascospores) were photographed using a Canon EOS 600D (Tokyo, Japan) digital camera mounted on a Nikon ECLIPSE 80i (Tokyo, Japan) compound microscope. All microscopic measurements were taken using the Tarosoft (R) Image Frame Work v.09, and the measurements were reported as minimum–maximum values and average values. Images were processed with Adobe Photoshop CS6 software v.13 (Adobe Systems, San Jose, CA, USA). Single-spore isolation was used to obtain pure cultures, following the methods described by Senanayake et al. (2020). Herbarium materials were deposited at the Cryptogams Kunming Institute of Botany, Academia Sinica (**HKAS**), Kunming, China, and living cultures were deposited at the Kunming Institute of Botany Culture Collection (**KUNCC**), Kunming, China. Faces of fungi (Jayasiri et al. 2015) and Index Fungorum (2026) numbers were obtained for the new taxa.

DNA extraction, PCR amplification, and sequencing

Genomic DNA was extracted from the mycelium grown on potato dextrose agar (PDA) at 25 °C for four weeks using Biospin Fungus Genomic DNA Extraction Kit (BioFlux®) (Hangzhou, P. R. China). Six gene regions, including internal transcribed spacer region (ITS), large subunit nuclear ribosomal (LSU), small subunit ribosomal RNA (SSU), translation elongation factor 1-alpha gene (*tef*1-α), RNA polymerase II second largest subunit (*rpb*2) and β-tubulin (*tub*2) were amplified with primers ITS5/ ITS4 (White et al. 1990), LR0R/ LR5 (Vilgalys and Hester 1990), NS1/ NS4 (White et al. 1990), 983F/ 2218R (Rehner and Buckley 2005), fRPB2-5F/ fRPB2-7cR (Liu et al. 1999) and T1/ T22 (O'Donnell and Cigelnik 1997), respectively. The PCR thermal cycle programs for SSU, LSU, ITS, *tef*1-α and *rpb*2 were set as described in Wanasinghe et al. (2021). The quality of PCR products was checked on 1% agarose gel electrophoresis stained with ethidium bromide. The PCR products were sent for sequencing at Tsingke Company, Kunming City, Yunnan Province, China. The sequences were deposited in GenBank.

Phylogenetic analyses

BLASTn searches were performed, and sequences showing high similarity were identified to determine their closest taxonomic matches. The sequences were downloaded from GenBank (http://www.ncbi.nlm.nih.gov/) based on the BLASTn results and recent publications (Huang et al. 2021; Zhang et al. 2021, 2023c, 2025; Sugita and Tanaka 2022; Chen et al. 2024; Crous et al. 2024; Leonardi et al. 2024; Habib et al. 2025; Lim et al. 2025; Luo et al. 2025). The newly generated sequences in this study were assembled by BioEdit 7.2.3 (Hall 1999). The individual gene regions were separately

aligned in MAFFT v.7 web server (http://mafft.cbrc.jp/alignment/server/) (Katoh et al. 2019). The alignments of each gene were improved by manually deleting the ambiguous regions plus gaps and combined using BioEdit 7.2.3. The final alignments were converted to NEXUS format (nxs) using Clustal X version 1.81 (Thompson et al. 1997) and processed for Bayesian and maximum parsimony analysis. The FASTA format was changed into PHY format via Alignment Transformation Environment (ALTER) online program (http://www.sing-group.org/ALTER/) and used for maximum likelihood (ML) analysis. The maximum likelihood (ML) analysis was performed on the CIPRES Science Gateway v.3.3 (http://www.phylo.org/portal2/; Miller et al. 2010) using RAxML-HPC2 on XSEDE v.8.2.12 (Stamatakis 2014) with parameters adjusted for 1000 bootstrap iterations and the GTRGAMMA substitution model. Bayesian inference was performed in MrBayes v.3.2.7a (Ronquist et al. 2012) using Markov chain Monte-Carlo sampling (BMC-MC) to determine posterior probabilities (PPs) (Rannala and Yang 1996). The model of evolution for each gene was estimated using MrModeltest v.2.3 (Nylander et al. 2008) via PAUP v.4.0b10 (Ronquist and Huelsenbeck 2003). Six simultaneous Markov chains were run for 2,000,000 generations, with trees sampled at every 200 generations, until it was stopped when the standard deviation of split frequencies between the two simultaneous runs dropped below 0.01. Phylogenetic trees were visualized with FigTree v.1.4.0 (Rambaut 2012) and edited using Microsoft PowerPoint and Adobe Illustrator® CS6 v.26.0 (Adobe Systems, San Jose, CA, USA).

Results

Taxonomy and phylogeny

Based on polyphasic approaches, a total of ten species were indentified, including three new species and seven new records, updated phylogenetic trees and descriptions for all these taxa are given below. The classification follows Hyde et al. (2024b) and Thiyagaraja et al. (2025).

Diaporthomycetidae Senan., Maharachch. & K.D. Hyde, 2015

Calosphaeriales M.E. Barr, Mycologia 75(1): 11 (1983)

Calosphaeriaceae Munk, Dansk bot. Ark. 17(no. 1): 278 (1957)

Notes. Calosphaeriaceae was originally established by Munk (1957) and has since undergone several taxonomic revisions (Damm et al. 2008; Réblová et al. 2015; Maharachchikumbura et al. 2016; Wijayawardene et al. 2018). Phylogenetic studies confirmed the inclusion of *Calosphaeria*, *Flabellascus*, *Jattaea*, and *Togniniella* within this family (Huang et al. 2021; Hyde et al. 2024b). Generally, Calosphaeriaceae species are saprobic, inhabiting dead wood and bark of various trees and shrubs. However, some species of *Jattaea* and *Calosphaeria* have also been associated with fruit trees, especially *Prunus* species, where they are implicated in cankers and necrotic lesions on woody tissues (Kazemzadeh-Chakusary et al. 2020). In this study, we introduced a new host record, *Jattaea algeriensis* from *Myrsine seguinii* (Myrsinaceae).

***Jattaea algeriensis* Berl., Icon. fung. (Abellini) 3(1–2): 6 (1900)**
Index Fungorum: IF215105
Facesoffungi Number: FoF10117
Fig. 2

Description. ***Saprobic*** on dead woody twigs. **Sexual morph:** ***Ascomata*** perithecia, 150–320 µm high × 135–430 µm diam. ($\bar{x}$ = 210 × 290 µm, n = 5), scattered, solitary on wood beneath the periderm, dark brown to black, multi-loculate, each locule 120–170 µm high × 140–190 µm diam. ($\bar{x}$ = 140 × 160 µm, n = 5), with small papilla on the host surface, with cylindrical neck, central or lateral. ***Ostioles*** 100–170 µm high × 40–70 µm diam. ($\bar{x}$ = 139 × 53 µm, n = 5), ostiolum periphysate. ***Peridium*** 8–15 µm thick, leathery, 3–5 layers of brown cells of ***textura angularis***. ***Paraphyses*** 2–3 µm wide, numerous, hyaline, filiform, unbranched, septate, guttulate, embedded in a gelatinous matrix, slightly tapering towards the apex, obtuse. ***Asci*** 20–32 × 5–6.3 µm ($\bar{x}$ = 27 × 5.5 µm, n = 20), 8-spored, unitunicate, short-stipitate, clavate, broadly rounded at the thickened apex, tapering towards the base. ***Ascospores*** 4.5–6.4 × 1.7–2.2 µm ($\bar{x}$ = 5.4 × 2 µm, n = 30), 2–3-seriate, aseptate, ellipsoidal to suballantoid, hyaline, 2-guttulate, smooth-walled. **Asexual morph:** Undetermined.

Culture characteristics. Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes are produced from the basal and apical cell of ascospore. Colonies on PDA, slow growth, reaching 15 mm diameter after one week at 20–25 °C, mycelia superficial, circular, fimbriate, flat, entire edge, white; reverse, yellowish.

Material examined. China • Yunnan Province, Lincang, (24°5'30"N, 100°5'33"E, elevation: 1557.5 m) on dead woody twigs of *Myrsine seguinii* (Myrsinaceae), 10 August 2020, G.C. Ren, LC21 (HKAS 122750), living culture KUNCC 21-0604.

Known distribution and hosts. Algeria, on decayed canes of *Rubus fruticosus* (Saccardo and Sydow 1902; Réblová 2011); South Africa, on wood of *Prunus salicina* (Damm et al. 2008; Réblová 2011); Iran, as pathogens derived from *Mespilus germanica* and *Parrotia persica* (Kazemzadeh-Chakusary et al. 2020); China, on dead woody twigs of *Myrsine seguinii* (Myrsinaceae) (this study).

GenBank numbers. ITS: PX568860, LSU: PX473152, *tef*1-α: PX521731.

Notes. *Jattaea algeriensis* was initially described by Saccardo and Sydow (1902) based on its sexual morphic characteristics. Later, Réblová (2011) synonymized *Jattaea prunicola* with *J. algeriensis* following detailed morphological analysis and phylogenetic studies. *Jattaea prunicola*, originally introduced by Damm et al. (2008), was distinguished by its sexual morph and a phialophora-like anamorph observed in pure culture. Recently, *J. algeriensis* was isolated from the necrotic woody tissues of *Mespilus germanica* and *Parrotia persica* in Iran, identified based on both asexual morph features and phylogenetic analysis (Kazemzadeh-Chakusary et al. 2020). According to the multi-gene phylogenetic analyses of combined LSU, ITS, TUB sequence dataset, our new isolate (KUNCC 21-0604) nested with *Jattaea algeriensis* (CBS 120871, STE-U 6399) with 90% ML and 0.95 BYPP bootstrap support (Fig. 1). Our new isolate (KUNCC 21-0604) shares similarities with *Jattaea algeriensis* (CBS 120871, MC 8938) in having perithecia, scattered, solitary, dark brown to black ascomata with papilla; brown cells of textura angularis peridium; unitunicate, clavate, short-stipitate asci; and

aseptate, suballantoid, hyaline ascospores. However, there are differences in ascospore and ascomata morphology, *Jattaea algeriensis* (CBS 120871, MC 8938) has hyaline to pale yellow-brown ascospores with an appendage at the base and uni-loculate ascomata, while our new isolate (KUNCC 21-0604) has hyaline ascospores without appendages and multi-loculate ascomata (Damm et al. 2008; Réblová 2011). Sequence comparison for the ITS and LSU region between our isolates (KUNCC 21-0604) and *J. algeriensis* (CBS 120871, STE-U 6399) showed no significant base pair differences. Therefore, we identified our taxon as a new host record of *J. algeriensis* from *Myrsine seguinii* (Myrsinaceae), and new geographic record in China.

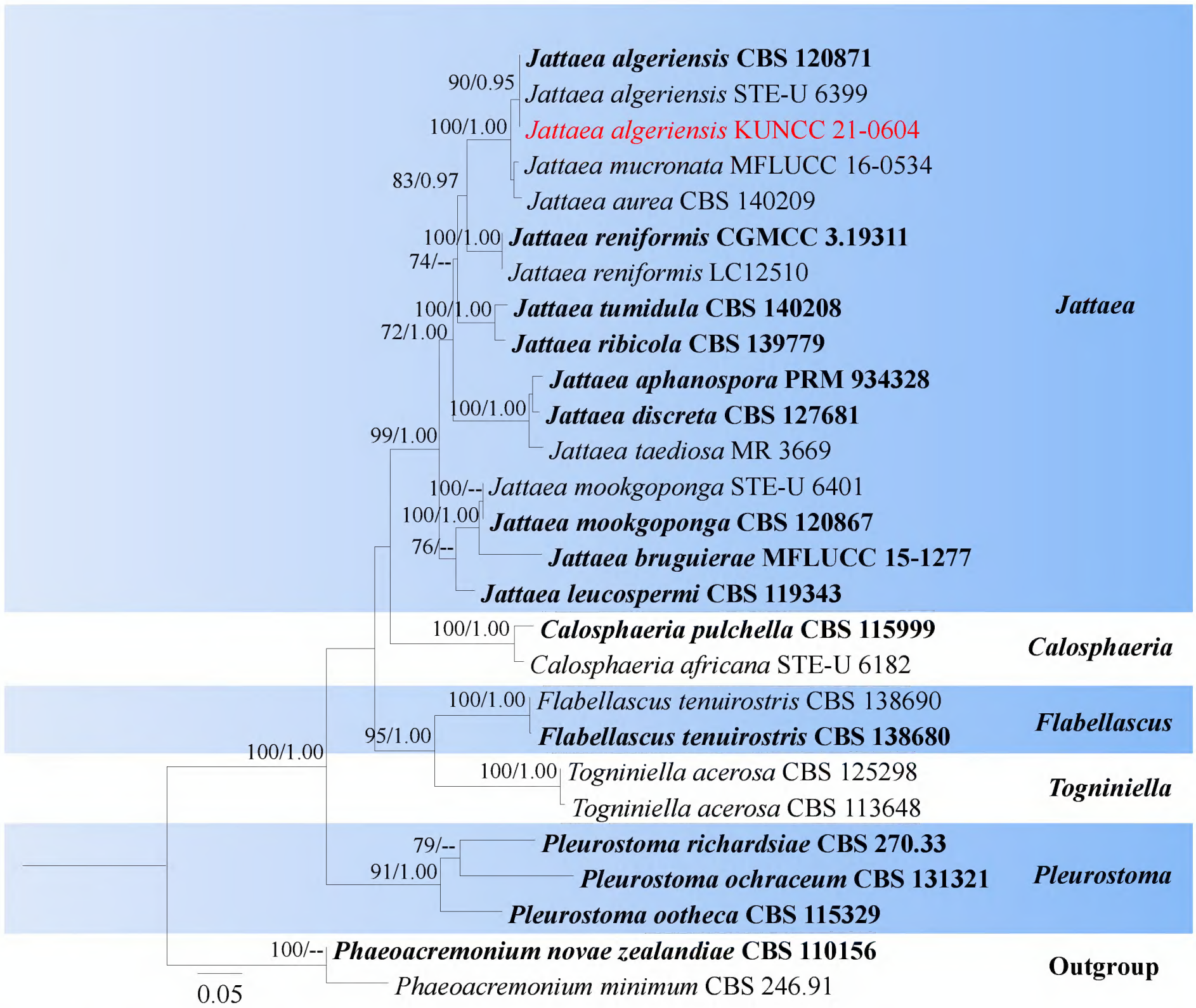

Figure 1. Phylogram generated from ML analysis based on LSU, ITS and TUB sequence data representing Calosphaeriaceae. Related sequences are obtained following Zhang et al. (2021). Twenty-seven strains are included in the combined analyses, which comprise 1834 characters for LSU, ITS and TUB alignment. *Phaeoacremonium novae zealandiae* (CBS 110156) and *P. minimum* (CBS 246.91) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -10057.676635 is presented. The matrix had 618 distinct alignment patterns, with 20.59% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.222567, C = 0.280141, G = 0.295349, T = 0.201943; substitution rates AC = 1.276096, AG = 2.336664, AT = 1.587462, CG = 0.904375, CT = 4.777312, GT = 1.0000. Gamma distribution shape parameter α = 0.182504 and tree-length = 1.960861. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and posterior probability values greater than 0.95 from BYPP analysis labelled on the nodes. Strains of the newly described species are in red, while type strains are in bold.

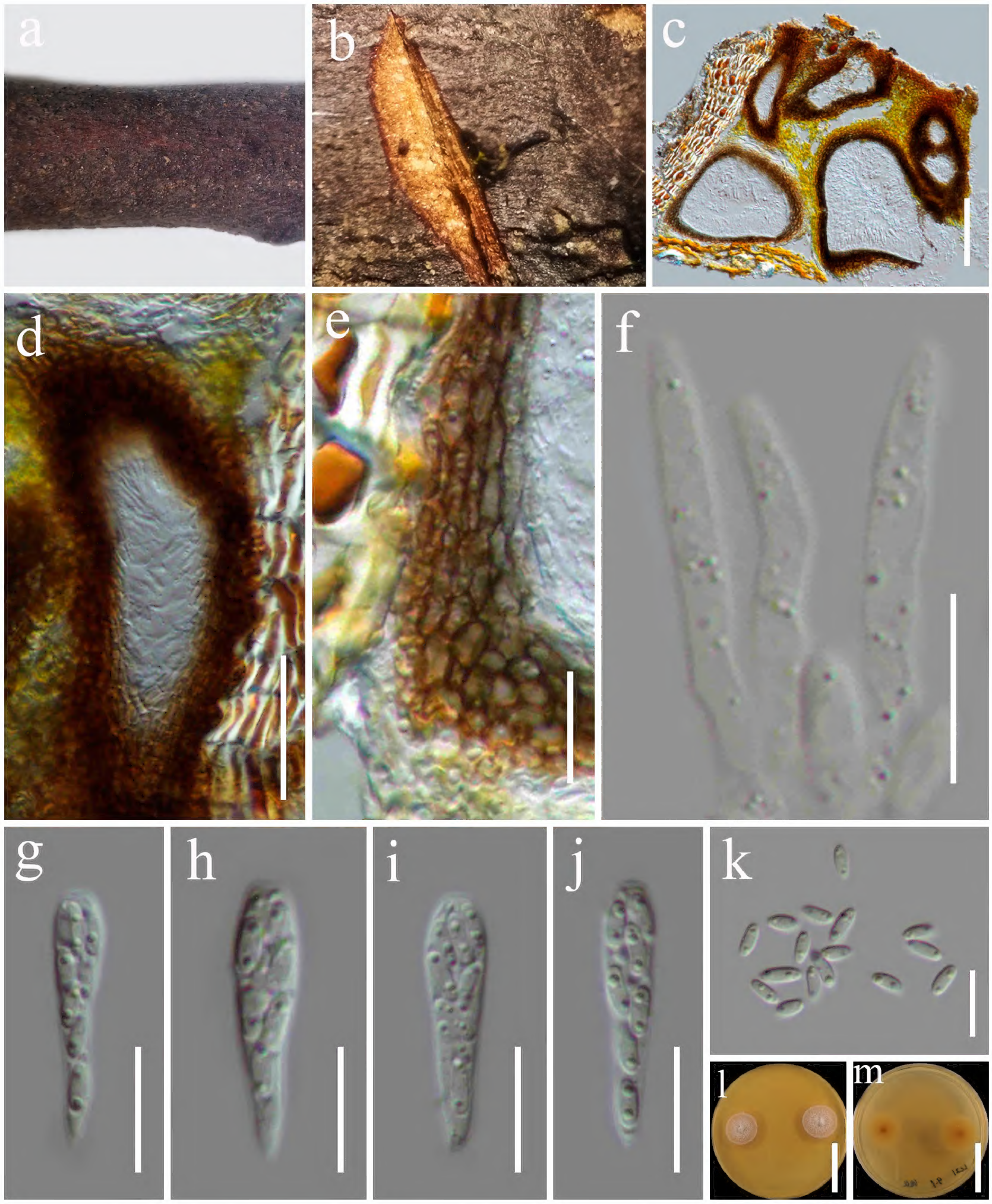

Figure 2. *Jattaea algeriensis* (HKAS 122750). **a, b.** Appearance of ascomata on host substrate; **c.** Section of ascoma; **d.** Section of ostiole; **e.** Peridium; **f.** Paraphyses; **g–j.** Asci; **k.** Ascospores; **l, m.** Culture characters on PDA (**l** from above; **m** from below). Scale bars: 100 μm (**c**); 50 μm (**d**); 10 μm (**e**); 10 μm (**f–k**); 20 mm (**l, m**).

Togniniales Senan., Maharachch. & K.D. Hyde, in Maharachchikumbura et al., Fungal Diversity 72: 220 (2015)

Togniniaceae Réblová, L. Mostert, W. Gams & Crous, Stud. Mycol. 50(2): 540 (2004)

Notes. Réblová et al. (2004) established Togniniaceae based on phylogenetic analysis of LSU and SSU sequence. The family include both sexual (*Conidiotheca* and *Togninia*) and asexual genera (*Phaeoacremonium*) (Réblová

and Mostert 2007). This family has been included in Calosphaeriales (Mostert et al. 2003) and Diaporthales (Mostert et al. 2006) based on morpho-molecular analysis. Maharachchikumbura et al. (2015) excluded it from Diaporthales and introduced it in Togniniales. Subsequent studies, including those by Hyde et al. (2020a) and Calabon et al. (2021), accepted both *Conidiotheca* and *Phaeoacremonium* within Togniniaceae. In contrast, more recent classifications by Wijayawardene et al. (2022) and Hyde et al. (2024b) recognize only *Phaeoacremonium* as a valid genus within the family.

***Phaeoacremonium camporesii* Wijes., Camporesi & K.D. Hyde, Fungal Diversity 114: 360 (2022)**

Index Fungorum: IF559245

Facesoffungi Number: FoF10568

Fig. 4

Description. ***Saprobic*** on dead woody twigs. **Sexual morph:** ***Ascomata*** 160–220 µm high, 180–360 µm diam. ($\bar{x}$ = 195 × 270 µm, n = 5), perithecial, immersed to semi-immersed, globose to subglobose, sometimes, truncate at the base, black, coriaceous, ostiolate. ***Peridium*** 10–36 µm thick, multi-layers of brown to dark brown cells of ***textura angularis***. ***Paraphyses*** comprising numerous, 2.5–4.5 µm wide, hyaline, branched, septate, slightly constricted at septa and gradually narrowed towards the apex. ***Asci*** 15–20 × 4–5 µm ($\bar{x}$ = 17 × 4.4 µm, n = 20), 8-spored, unitunicate, clavate, apex truncate, rounded at the base, apedicellate. ***Ascospores*** 4.4–5.3 × 1–1.4 µm ($\bar{x}$ = 4.6 × 1.2 µm, n = 30), biseriate, allantoid, reniform with rounded ends, unicellular, hyaline, thin-walled, smooth-walled, often containing small guttules at both ends. **Asexual morph:** Undetermined.

Culture characteristics. Ascospores germinating on PDA within 24 h at room temperature (25 °C). Colonies on PDA, reaching 50–55 mm diameter after one week at 20–25 °C, mycelia superficial, flat, velvety, white, umbonate at center; reverse, white, pale yellow at the center.

Material examined. China • Yunnan Province, Lincang (24°5'30"N, 100°5'33"E, elevation: 1558 m) on dead woody twigs of *Calophyllum polyanthum* (Calophyllaceae), 12 July 2020, G.C. Ren, LC31 (HKAS 122752), living culture KUNCC 21-0608.

Known distribution and hosts. Italy, on dead aerial branch of *Corylus avellana* (Phukhamsakda et al. 2022); Iran, on necrotic wood tissues of *Tamarix ramosissima* (Rahimi-Nia et al. 2025); China, on dead branch of *Calophyllum polyanthum* (Calophyllaceae) (this study).

GenBank numbers. ITS: PP663079, LSU: PP663086, SSU: PX583841.

Notes. *Phaeoacremonium* was established by Crous et al. (1996), with *P. parasiticum* designated as the type species. Currently, 73 species are recognized within the genus (Calabon et al. 2024; Mostert et al. 2024; Lim et al. 2025; Zhang et al. 2025). Multi-locus phylogenetic analyses based on a concatenated dataset of ITS, TUB, ACT, *tef*1-α, and LSU sequences revealed that our new collection (KUNCC 21-0608) is closely related to *Phaeoacremonium camporesii* (MFLUCC 21-0224), with strong statistical support (100% ML/ 1.00 BYPP; Fig. 3). Comparative analysis of the ITS and TUB sequences between our isolate (KUNCC 21-0608) and the ex-type strain of *P. camporesii* (MFLUCC 21-0224) revealed a 5.4% difference in the TUB region (17/ 313 bp, without gaps),

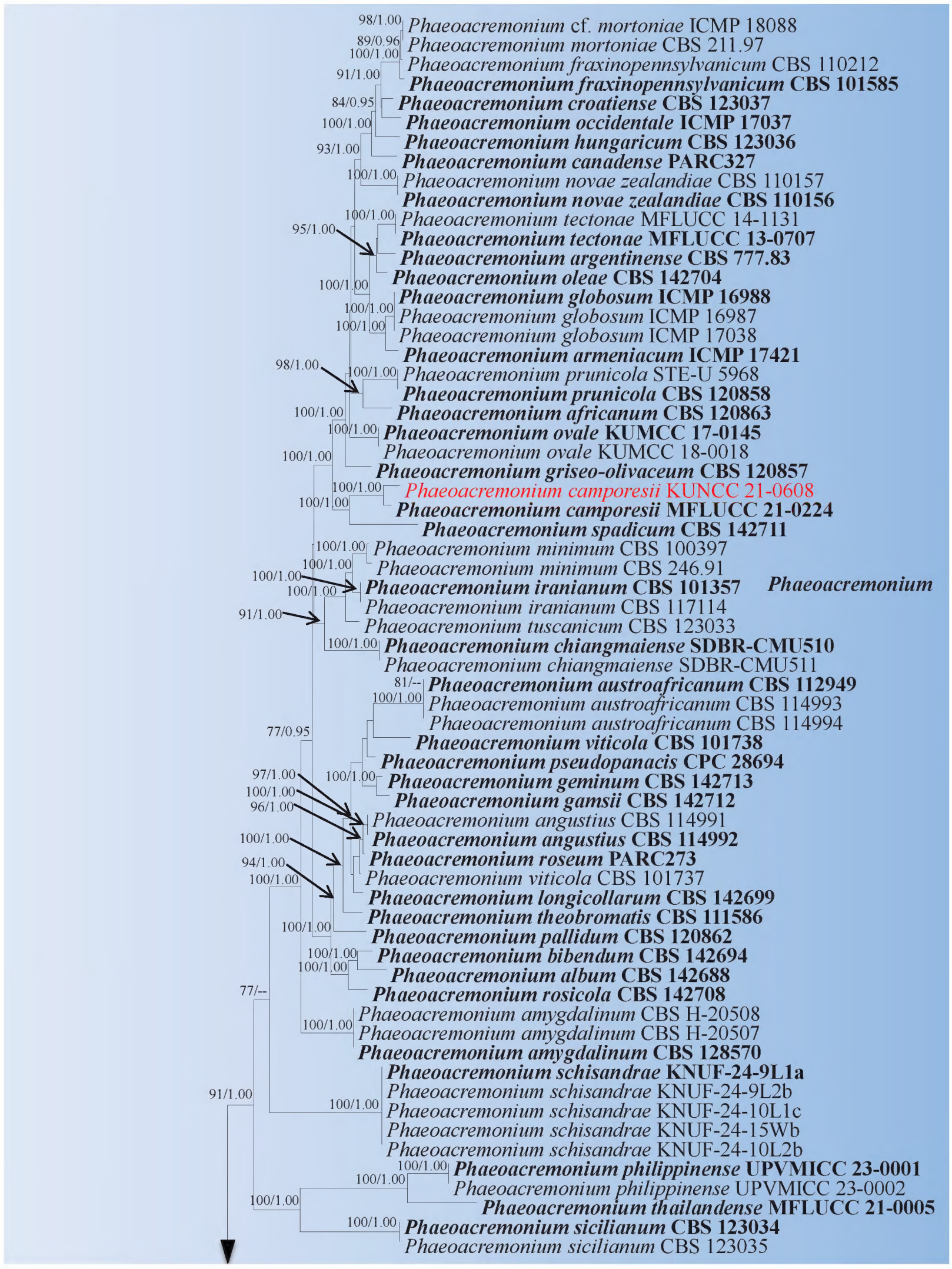
98/1.00 Phaeoacremonium cf. mortoniae ICMP 18088
89/0.96 Phaeoacremonium mortoniae CBS 211.97
100/1.00 Phaeoacremonium fraxinopennsylvanicum CBS 110212
91/1.00 Phaeoacremonium fraxinopennsylvanicum CBS 101585
84/0.95 Phaeoacremonium croatiense CBS 123037
100/1.00 Phaeoacremonium occidentale ICMP 17037
93/1.00 Phaeoacremonium hungaricum CBS 123036
Phaeoacremonium canadense PARC327
100/1.00 Phaeoacremonium novae zealandiae CBS 110157
Phaeoacremonium novae zealandiae CBS 110156
100/1.00 Phaeoacremonium tectonae MFLUCC 14-1131
95/1.00 Phaeoacremonium tectonae MFLUCC 13-0707
Phaeoacremonium argentinense CBS 777.83
Phaeoacremonium oleae CBS 142704
100/1.00 Phaeoacremonium globosum ICMP 16988
100/1.00 Phaeoacremonium globosum ICMP 16987
100/1.00 Phaeoacremonium globosum ICMP 17038
Phaeoacremonium armeniacum ICMP 17421
98/1.00 100/1.00 Phaeoacremonium prunicola STE-U 5968
Phaeoacremonium prunicola CBS 120858
100/1.00 Phaeoacremonium africanum CBS 120863
100/1.00 Phaeoacremonium ovale KUMCC 17-0145
100/1.00 Phaeoacremonium ovale KUMCC 18-0018
Phaeoacremonium griseo-olivaceum CBS 120857
100/1.00 Phaeoacremonium camporesii KUNCC 21-0608
100/1.00 Phaeoacremonium camporesii MFLUCC 21-0224
Phaeoacremonium spadicum CBS 142711
100/1.00 Phaeoacremonium minimum CBS 100397
100/1.00 Phaeoacremonium minimum CBS 246.91
100/1.00 Phaeoacremonium iranianum CBS 101357
100/1.00 Phaeoacremonium iranianum CBS 117114
91/1.00 Phaeoacremonium tuscanicum CBS 123033
100/1.00 Phaeoacremonium chiangmaiense SDBR-CMU510
Phaeoacremonium chiangmaiense SDBR-CMU511
81/-- Phaeoacremonium austroafricanum CBS 112949
100/1.00 Phaeoacremonium austroafricanum CBS 114993
Phaeoacremonium austroafricanum CBS 114994
77/0.95 Phaeoacremonium viticola CBS 101738
Phaeoacremonium pseudopanacis CPC 28694
97/1.00 100/1.00 Phaeoacremonium geminum CBS 142713
100/1.00 Phaeoacremonium gamsii CBS 142712
96/1.00 Phaeoacremonium angustius CBS 114991
100/1.00 Phaeoacremonium angustius CBS 114992
Phaeoacremonium roseum PARC273
94/1.00 Phaeoacremonium viticola CBS 101737
100/1.00 Phaeoacremonium longicollarum CBS 142699
Phaeoacremonium theobromatis CBS 111586
100/1.00 Phaeoacremonium pallidum CBS 120862
100/1.00 Phaeoacremonium bibendum CBS 142694
100/1.00 Phaeoacremonium album CBS 142688
77/-- Phaeoacremonium rosicola CBS 142708
Phaeoacremonium amygdalinum CBS H-20508
100/1.00 Phaeoacremonium amygdalinum CBS H-20507
Phaeoacremonium amygdalinum CBS 128570
Phaeoacremonium schisandrae KNUF-24-9L1a
91/1.00 Phaeoacremonium schisandrae KNUF-24-9L2b
100/1.00 Phaeoacremonium schisandrae KNUF-24-10L1c
Phaeoacremonium schisandrae KNUF-24-15Wb
Phaeoacremonium schisandrae KNUF-24-10L2b
100/1.00 Phaeoacremonium philippinense UPVMICC 23-0001
100/1.00 Phaeoacremonium philippinense UPVMICC 23-0002
100/1.00 Phaeoacremonium thailandense MFLUCC 21-0005
100/1.00 Phaeoacremonium sicilianum CBS 123034
Phaeoacremonium sicilianum CBS 123035
Phaeoacremonium

Figure 3. Phylogram generated from ML analysis based on ITS, TUB, ACT, *tef*1-α and LSU sequence data representing *Phaeoacremonium*. Related sequences are obtained following Lim et al. (2025) and Zhang et al. (2025). One hundred and eighteen strains are included in the combined analyses, which comprise 2630 characters for ITS, TUB, ACT, *tef*1-α and LSU alignment. *Flabellascus tenuirostris* (CBS 138680) and *Jattaea algeriensis* (STE-U 6201) were used as the out-group taxa. The best-scoring RAxML tree with a final likelihood value of -29974.772558 is presented. The matrix had 1369 distinct alignment patterns, with 47.07% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.222379, C = 0.293334, G = 0.251529, T = 0.232759; substitution rates AC = 1.395429, AG = 3.734177, AT = 1.396244, CG = 1.142111, CT = 4.959406, GT = 1.0000. Gamma distribution shape parameter α = 0.286131 and tree-length = 4.360818. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and posterior probability values greater than 0.95 from BYPP analysis labelled on the nodes. Strains of the newly described species are in red, while type strains are in bold.

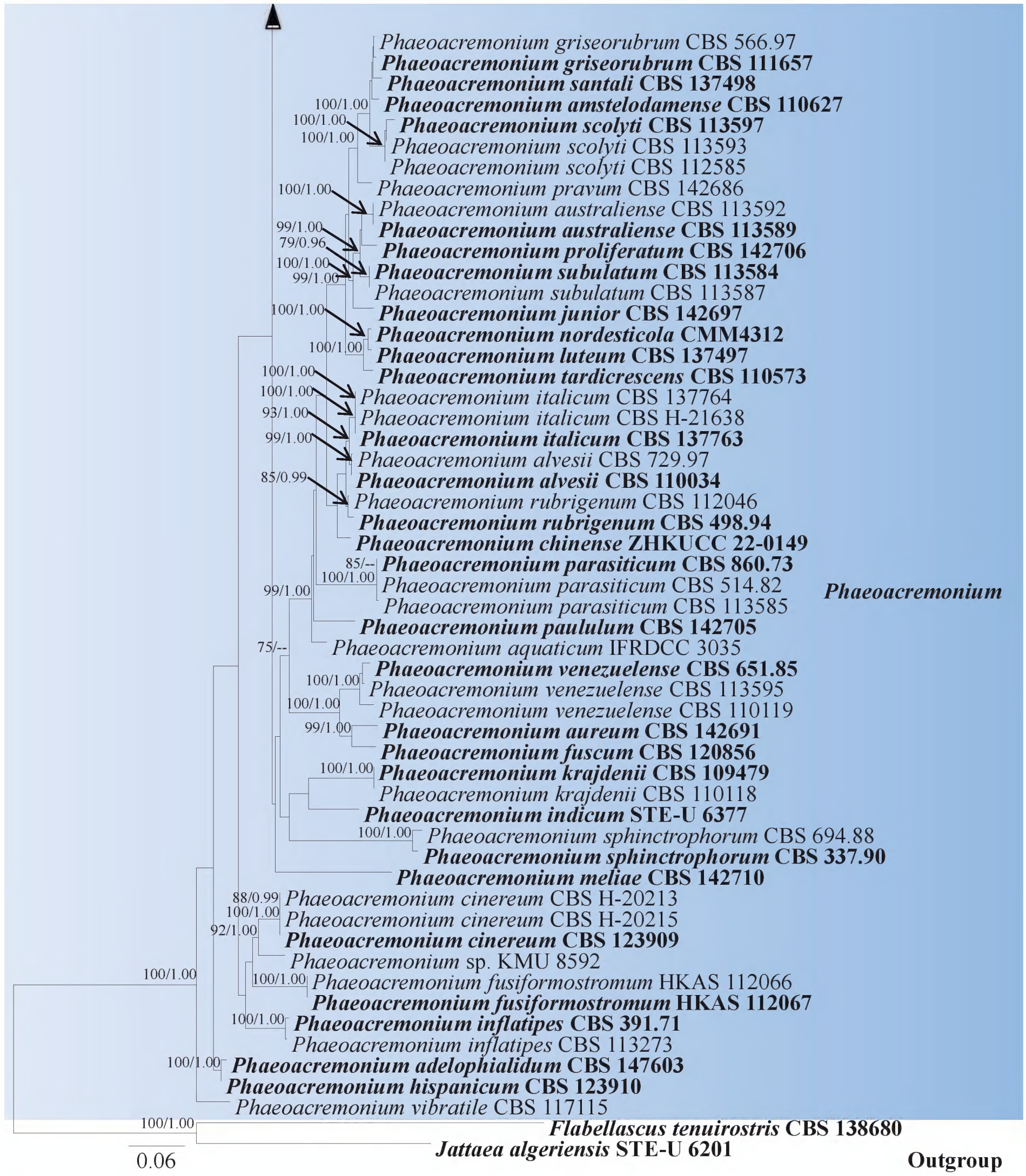

Figure 3. Continued.

while no significant differences were observed in the ITS region. Morphologically, our new isolate (KUNCC 21-0608) shares similarities with *P. camporesii* in having perithecia, immersed to semi-immersed, globose to subglobose ascomata; unitunicate, 8-spored, clavate asci with a truncate apex; and biseriate, allantoid to reniform, unicellular, hyaline, thin- and smooth-walled ascospores with rounded ends. Based on both molecular and morphological evidence, we identify KUNCC 21-0608 as a new host record of *Phaeoacremonium camporesii*, collected from *Calophyllum polyanthum* (Calophyllaceae) in China.

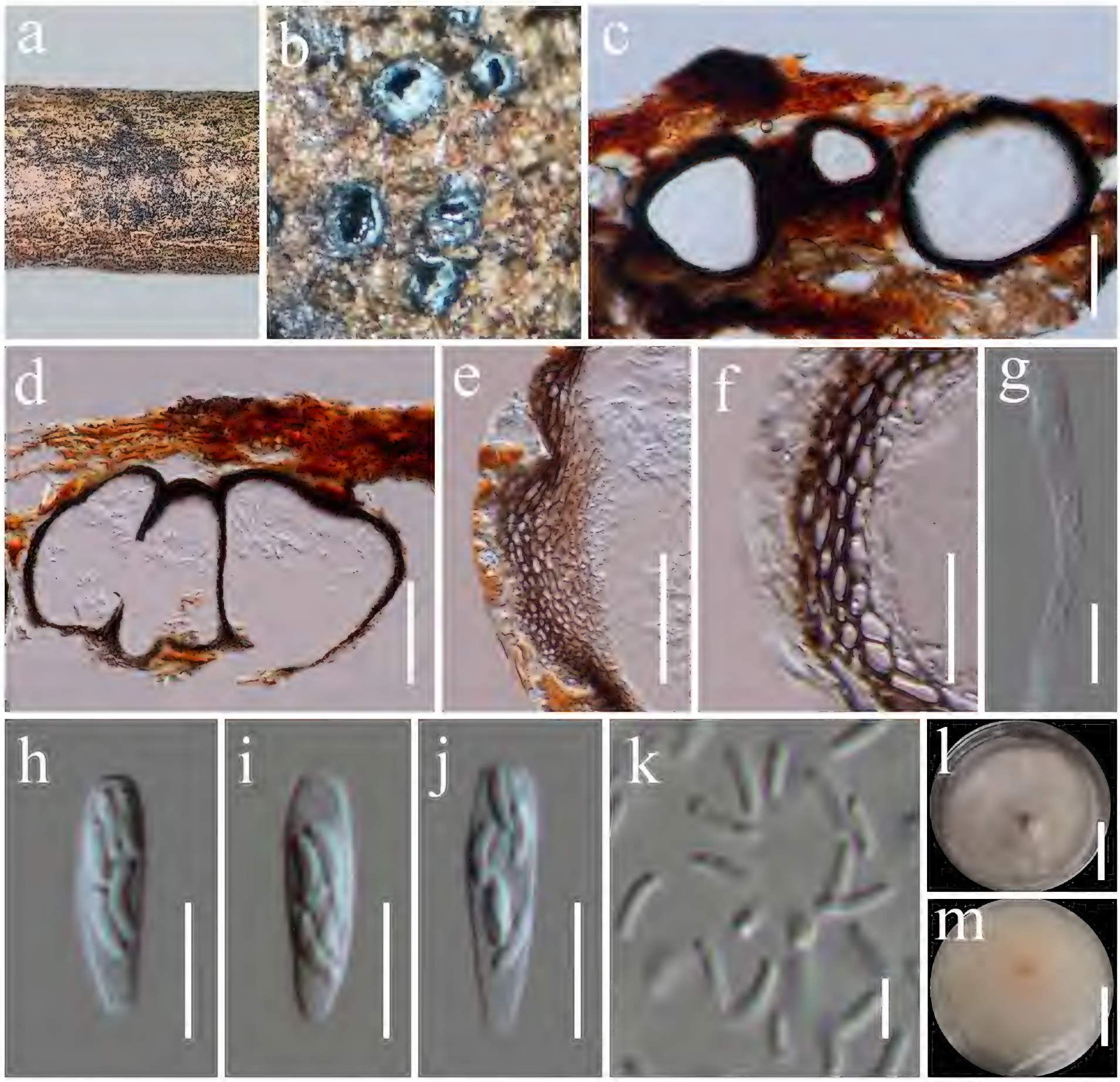

Figure 4. *Phaeoacremonium camporesii* (HKAS 122752). **a.** Appearance of ascomata on host substrate; **b.** Ascomata in transverse section; **c, d.** Sections of ascomata; **e, f.** Peridium; **g.** Paraphyses; **h–j.** Asci; **k.** Ascospores; **l, m.** Culture characters on PDA (**l** from above, **m** from below). Scale bars: 100 μm (**c–e**); 10 μm (**f–j**); 5 μm (**k**); 20 mm (**l, m**).

Thyridiales R. Sugita & Kaz. Tanaka, MycoKeys 86: 156 (2022)

Thyridiaceae J.Z. Yue & O.E. Erikss., Syst. Ascom. 6(2): 233 (1987)

Notes. Thyridiaceae was established by Yue and Eriksson (1987) with *Thyridium vestitum* designated as the type species. For a long time, the family was treated as Sordariomycetes *incertae sedis* until Sugita and Tanaka (2022) established a new order, Thyridiales, within Sordariomycetes to accommodate Thyridiaceae. Members of Thyridiaceae are saprobic or hemibiotrophic on woody substrates, with some species occurring as endophytes notably, there are no reports of pathogenic species in this family (Hyde et al. 2020a). At present, Thyridiaceae comprises two genera, *Thyridium* and *Phialemoniopsis* (Hyde et al. 2020b, 2024b).

***Thyridium tiliae* Crous & Akulov, Fungal Syst. Evol. 14: 427 (2024)**
Index Fungorum: IF856106
Facesoffungi Number: FoF18852
Fig. 6

Description. ***Saprobic*** on dead woody twigs. **Sexual morph:** ***Stromata*** scattered to grouped, subepidermal, immersed to erumpent, with interwoven yellowish or black tomentum. ***Ascomata*** 290–520 µm high, 300–530 µm diam. ($\bar{x}$ = 410 × 430 µm, n = 5), mostly grouped, immersed in stromata to erumpent through host surface. ***Peridium*** 20–30 µm thick, composed of several layers of thick-walled, dark brown cell of ***textura angularis***. ***Ostiolar*** neck cylindrical, short or long, separated or convergent in upper stromata. ***Paraphyses*** 3–5.4 µm wide, numerous, septate, unbranched, hyaline, cylindrical. ***Asci*** 130–160 × 15–21 µm ($\bar{x}$ = 148.3 × 18.3 µm, n = 20), 8-spored, unitunicate, cylindrical, rounded at the apex, with a short pedicel. ***Ascospores*** 20–23 × 8–11.3 µm ($\bar{x}$ = 21 × 10 µm, n = 30), muriform, ellipsoid, hyaline when immature, becoming dark brown at maturity, with 3 transverse septa and 1 longitudinal septum, thickened, and pigmented at the septa. **Asexual morph:** Undetermined.

Culture characteristics. Ascospores germinating on PDA within 24 h at room temperature (25 °C). Colonies on PDA, reaching 50–55 mm diameter after one week at 20–25 °C, mycelia superficial, flat, fimbriate, pale yellow, some hyphae are embedded in the culture medium; reverse, pale yellow.

Material examined. China • Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Jinghong (21°55.19'N, 101°15.24'E, elevation: 522 m), on dead woody twigs of *Pellacalyx yunnanensis* (Rhizophoraceae), 4 March 2020, G. C. Ren, JH43 (HKAS 122742), living culture KUNCC 21-0586.

Known distribution and hosts. Ukraine, on dead twigs of *Tilia* sp. (Tiliaceae) (Crous et al. 2024); China, on dead woody twigs of *Pellacalyx yunnanensis* (Rhizophoraceae) (This study).

GenBank numbers. ITS: PP663078, LSU: PP663085, SSU: PX583842, *tef*1-α: PX521732.

Notes. The genus *Thyridium* was introduced by Nitschke (1867), with *T. vestitum* as the type species (Esfandiari and Petrak 1950). Currently, 51 species are listed in Species Fungorum (31 January 2026), occurring on various plants as saprobic or hemibiotrophic fungi (Crous et al. 2024), DNA sequences are only available for 18 species. Multi-loci phylogenetic analyses based on a concatenated LSU, ITS, ACT, *tef*1-α and TUB sequence dataset show that our new collections (KUNCC 21-0586) formed a close relationship with *Thyridium tiliae* (CPC 45933) as the basal lineage within the genus (98% ML/ 1.00 BYPP; Fig. 5). Comparative analysis of the ITS, LSU and *tef*1-α sequence data between our isolate KUNCC 21-0586 and *T. tiliae* (CPC 45933, ex-type) revealed nucleotide differences of 0.9% (5/ 546 bp, without gaps), 0.6% (5/ 811 bp, without gaps), and 3.9% (34/ 883 bp, without gaps), respectively. Morphologically, our collection *T. tiliae* shares several morphological features, including scattered stromata, perithecial ascomata immersed in stromata, cylindrical and septate paraphyses, unitunicate cylindrical asci with 8 spores, and septate ascospores (Crous et al. 2024). Based on both molecular and morphological evidence, we identify KUNCC 21-0586 as a new host record of *Thyridium tiliae*, collected from *Pellacalyx yunnanensis* (Rhizophoraceae) in China.

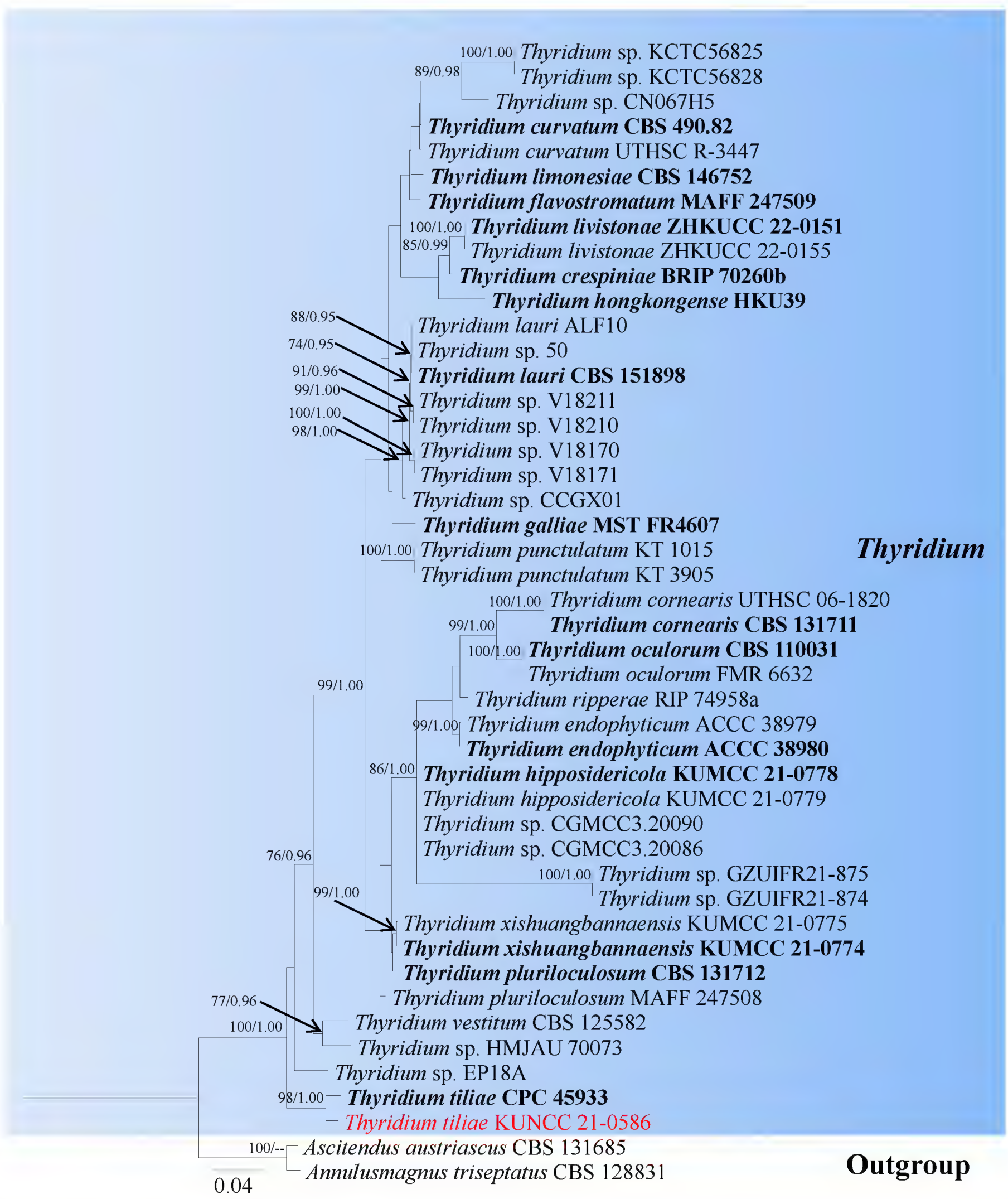

Figure 5. Phylogram generated from ML analysis based on LSU, ITS, ACT, *tef*1-α and TUB sequence data representing *Thyridium*. Related sequences are obtained following Sugita and Tanaka (2022), Leonardi et al. (2024) and Crous et al. (2024). Forty-six strains are included in the combined analyses, which comprise 2630 characters for LSU, ITS, ACT, *tef*1-α and TUB alignment. *Ascitendus austriascus* (CBS 131685) and *Annulusmagnus triseptatus* (CBS 128831) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -11734.391258 is presented. The matrix had 812 distinct alignment patterns, with 48.23% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.226472, C = 0.271383, G = 0.262638, T = 0.239508; substitution rates AC = 1.067369, AG = 2.011680, AT = 1.164926, CG = 1.259845, CT = 6.000431, GT = 1.0000. Gamma distribution shape parameter α = 0.171126 and tree-length = 0.987258. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and posterior probability values greater than 0.95 from BYPP analysis labelled on the nodes. Strains of the newly described species are in red, while type strains are in bold.

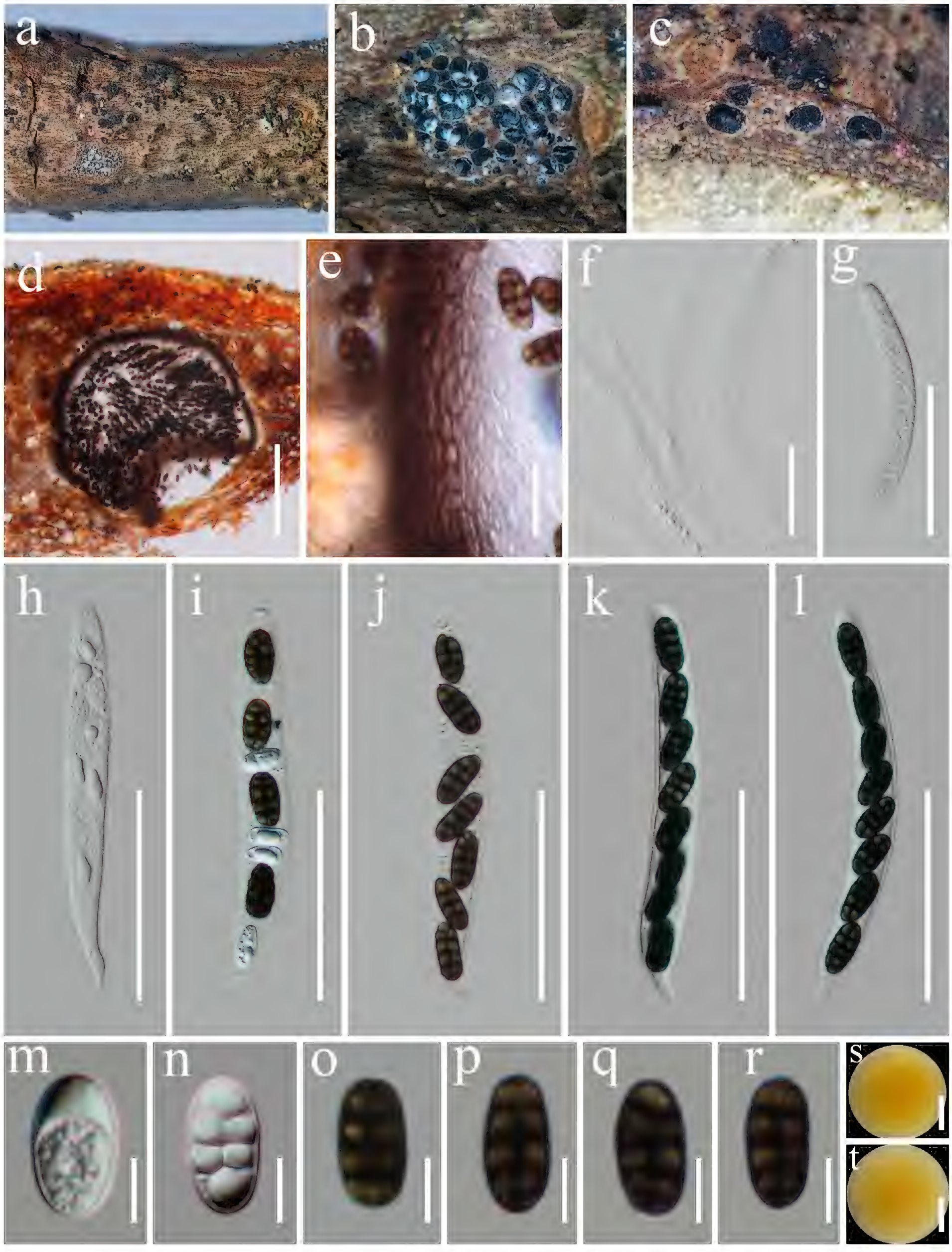

Figure 6. *Thyridium tiliae* (HKAS 122742). **a.** Appearance of ascomata on the host substrate; **b, c**. Ascomata in transverse section; **d.** Section of an ascoma; **e.** Peridium; **f.** Paraphyses; **g–l.** Asci; **m–r.** Ascospores; **s, t.** Culture characters on PDA (**s** from above; **t** from below). Scale bars: 200 μm (**d**); 200 μm (**e, f**); 100 μm (**g–l**); 10 μm (**m–r**); 20 mm (**s, t**).

Sordariomycetidae O.E. Erikss. & Winka, 1997
Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández, 2004

Linocarpaceae S. Konta & K.D. Hyde, Mycosphere 8(10): 1962 (2017)

Notes. Linocarpaceae was established by Konta et al. (2017) to accommodate two genera, *Linocarpon* (the type genus) and *Neolinocarpon*, based on morphological characteristics and multigene phylogenetic analyses using ITS and LSU sequences. This was placed in Chaetosphaeriales based on phylogenetic evidence. Later, Xu et al. (2020) introduced a third genus, *Claviformispora*, into Linocarpaceae, supported by both morphological features and phylogenetic analyses of LSU, SSU and *tef*1-α. *Claviformispora* currently comprises one species, *Linocarpon* 45 species and *Neolinocarpon* 14 species (Luo et al. 2025; Index Fungorum 2026). Species of *Linocarpon* and *Neolinocarpon* are characterized by narrow and long filiform, hyaline ascospores, often with refringent bands. In contrast, *Claviformispora* is distinguished by its clavate ascospores and a bambusicolous habitat (Xu et al. 2020). Linocarpaceae species are associated with plants as saprobes or endophytes and widely distributed (Zhang et al. 2023a).

***Neolinocarpon lincangense* G.C. Ren & Wanas., sp. nov.**
Index Fungorum: IF904525
Facesoffungi Number: FoF18853
Fig. 8

Etymology. The epithet reflects the location where the holotype was collected.

Holotype. HKAS 122751.

Description. ***Saprobic*** on dead woody twigs. **Sexual morph:** ***Ascomata*** 190–440 µm high, 400–540 µm diam. ($\bar{x}$ = 330 × 480 µm, n = 5), solitary to gregarious, immersed to semi-immersed, becoming raised to erumpent through the host tissue, globose to subglobose, carbonaceous, black, papillate. ***Ostiolar canal*** 60–120 µm wide, 100–260 µm long, central, cylindrical, straight, periphysate. ***Peridium*** 10–18 µm wide, outer cells fused with the host epidermal cells, thickness on both sides, composed of dark brown outer layer and hyaline inner layer comprising, thick-walled cells of ***textura angularis***. ***Hamathecium*** 3.5–6.5 µm wide, comprising dense, hyaline, septate, unbranched, filamentous, tapering towards the apex, slightly constricted at the septum, verruculose or guttule. ***Asci*** 100–120 × 8–13.5 µm ($\bar{x}$ = 110 × 10.7 µm, n = 20), 8-spored, unitunicate, with a wedge-shaped, J- subapical ring, cylindrical, long pedicellate, thin-walled. ***Ascospores*** 82–92 × 2–3 µm ($\bar{x}$ = 88.7 × 2.5 µm, n = 30), parallel in ascus, fasciculate, filiform, hyaline, aseptate, mostly curved, containing refringent septum-like bands, tapering towards the base and with a narrow-rounded apex, smooth-walled. **Asexual morph:** Undetermined.

Culture characteristics. Ascospores germinating on PDA within 24 h at room temperature. Colonies on PDA, reaching 15–20 mm diameter after one week at

20–25 °C, mycelia superficial, circular, flat, fimbriate, entire edge, white at the margin, gray white at the center; reverse, yellowish at the margin, dark brown at the center.

Material examined. CHINA • Yunnan Province, Lincang (24°5'30"N, 100°5'33"E, elevation: 1557.49 m) on dead woody twigs of *Knema furfuracea* (Myristicaceae), 12 July 2020, G.C. Ren, LC27 (holotype, HKAS 122751), ex-type culture KUNCC 21-0607.

GenBank numbers. LSU: PP663084.

Notes. The genus *Neolinocarpon* was introduced to accommodate linocarpon-like species by Hyde (1992), with *N. globosicarpum* as the type species. Recently, Habib et al. (2025) describe a new species, *Neolinocarpon huaxiense*, found on dead bamboo culms. Currently, 15 species are listed in Index Fungorum (2026). Except for *Neolinocarpon arengae*, *N. enshiense*, *N. phayaoense* and *N. rachidis*, sequence data are available in GenBank. Multi-loci phylogenetic analyses based on a concatenated SSU, LSU, ITS, and *tef*1-α sequence dataset show that our strain (KUNCC21-0607) is clustered with *Neolinocarpon* species (Fig. 1). The morphological characteristics of *Neolinocarpon lincangense* is similar to other species by its immersed ascomata with an ostiole, cylindrical asci with a wedge-shaped, J-, and subapical ring and filiform ascospores (Senwanna et al. 2018). However, *Neolinocarpon arengae*, *N. australiense*, *N. calami*, *N. enshiense*, *N. eutypoides*, *N. globosicarpum*, *N. rachidis* differs from our collection by the mucilaginous appendage (Hyde 1992; Hyde et al. 1998; Konta et al. 2017; Senwanna et al. 2018). The other six *Neolinocarpon* species differ from our new collection: *N. attaleae* has filiform -fusoid to clavate ascospores, *N. inconspicuum* has inconspicuous ascomata, *N. nonappendiculatus* has comparatively larger ascospores (114–138 × 2–2.5 µm), *N. nypicola* has immersed fruiting bodies, beneath light brown circular regions with a blackened outline, with 1–4 ostioles, *N. pennies* has comparatively smaller ascospores ((52) 57–64 (-84) × 2.5–3), *N. phayaoense* has hyaline to pale brown ascospores, and tapering towards the base (Hyde et al. 1998; Hyde and Alias 1999; Bhilabutra et al. 2006; Vitoria et al. 2013; Senwanna et al. 2018). Therefore, we identify our collection as a new species from Yunnan Province, China.

Neoleptosporellaceae J.F. Zhang, Y.Y. Chen & Jian K. Liu, Fungal Diversity 122: 110 (2023)

Notes. Neoleptosporellaceae was introduced by Zhang et al. (2023a) to accommodate *Neoleptosporella* as the type genus. Members of Neoleptosporellaceae are saprobes and they are reported on various plant hosts in tropical and temperate regions (Phukhamsakda et al. 2020; Hyde et al. 2020a; Zhang et al. 2023a, 2024). The sexual morph is characterized by solitary and immersed, brown to black, coriaceous, and subglobose to depressed globose ascomata, the asci remain unitunicate and broadly cylindrical, possessing a pedicellate form along with a J-, wedge-shaped, subapical ring. The ascospores are fasciculate, fusiform, C-shaped, or sigmoid configurations, non-septate, with acute ends and a guttulate appearance (Zhang et al. 2023a). The asexual morph of the family has not been observed.

Neoleptosporella camporesiana **R.H. Perera & K.D. Hyde, Fungal Diversity 100: 219 (2020)**

Index Fungorum: IF556898

Facesoffungi Number: FoF06962

Fig. 9

Description. ***Saprobic*** on dead woody twigs. **Sexual morph:** Appearing as shiny black, raised dome-shaped spots, with a central short papilla. ***Ascomata*** 180–250 µm high, 195–300 µm diam. ($\bar{x}$ = 220 × 250 µm, n = 5), solitary or aggregated, immersed beneath small clypeus appearing as a disc around the neck, uni-loculate, subglobose to depressed globose, ostiolate. ***Peridium*** 6–10 µm wide, outer cells fused with the host epidermal cells, composed of dark brown cells of ***textura angularis***. ***Paraphyses*** 3–7 µm diam., hyaline, branched, septate. ***Asci*** 75–100 × 7–9 µm ($\bar{x}$ = 82 × 8 µm, n = 20), 8-spored, unitunicate, cylindrical, short pedicellate, apex rounded with a wedge-shaped, J- apical ring. ***Ascospores*** 60–74 × 2.1–2.6 µm ($\bar{x}$ = 58 × 2.3 µm, n = 30), fasciculate, parallel becoming spiral at maturity, fliform, straight or curved, hyaline, aseptate, rounded at the apex, pointed at the base, smooth-walled, without appendages. **Asexual morph:** Undetermined.

Culture characteristics. Ascospores germinating on PDA within 24 h at room temperature (25 °C). Colonies on PDA, reaching 30–40 mm diameter after one week at 20–25 °C, mycelia superficial, circular, flat, fimbriate, entire edge, white; reverse, white.

Material examined. China • Yunnan Province, Lincang (24°5'30"N, 100°5'33"E, elevation: 1557.49 m), on dead woody twigs of *Castanopsis mekongensis* (Fagaceae), 12 July 2020, G.C. Ren, LC40 (HKAS 122881), living culture KUNCC 21-0612; • *ibid*., Xianggelila, tacheng (27°25'30"N, 99°50'44"E, elevation: 3190 m), on dead woody twigs of *Sorbus rehderiana* (Rosaceae), 1 September 2020, G.C. Ren, T709 (HKAS 122885), living culture KUNCC 21-0655.

Known distribution and hosts. Thailand (Hyde et al. 2020a; Phukhamsakda et al. 2020; Chaiwan et al. 2021), China (Manawasinghe et al. 2022; Chethana et al. 2023; this study). On dead stems of *Clematis subumbellata* (Phukhamsakda et al. 2020), dead branch of an unidentified plant (Hyde et al. 2020a; Chethana et al. 2023), dead stem of *Heteropanax fragrans* (Manawasinghe et al. 2022) and *Dracaena* sp. (Jayasiri et al. 2015), on dead woody twigs of *Castanopsis mekongensis* (Fagaceae) and *Sorbus rehderiana* (Rosaceae) (This study).

GenBank numbers. KUNCC 21-0612: ITS: PX568861, LSU: PX473153, SSU: PX583843, *tef*1-α: PX521733. KUNCC 21-0655: ITS: PX568862, LSU: PX473154, *tef*1-α: PX521734.

Notes. *Neoleptosporella* was proposed by Phukhamsakda et al. (2020) and typified with *N. clematidis*. Four species are accepted in *Neoleptosporella*, *Neoleptosporella camporesiana*, *N. clematidis*, *N. fusiformispora*, *N. palmae* (Hyde et al. 2020a; Phukhamsakda et al. 2020; Zhang et al. 2023a; Zhang et al. 2024). According to the multi-gene phylogenetic analyses of combined SSU, LSU, ITS, and *tef*1-α sequence dataset, our new isolates (KUNCC 21-0612, KUNCC 21-0655) nested with the strains of *Neoleptosporella camporesiana* (ZHKUCC 22-0218, MFLUCC 15-1016, Tak33) with 100% ML and 1.00 BYPP bootstrap support (Fig. 7). Our collection is morphologically similar to *Neoleptosporella camporesiana* in having ascomata with black shiny ostioles, cylindrical asci with

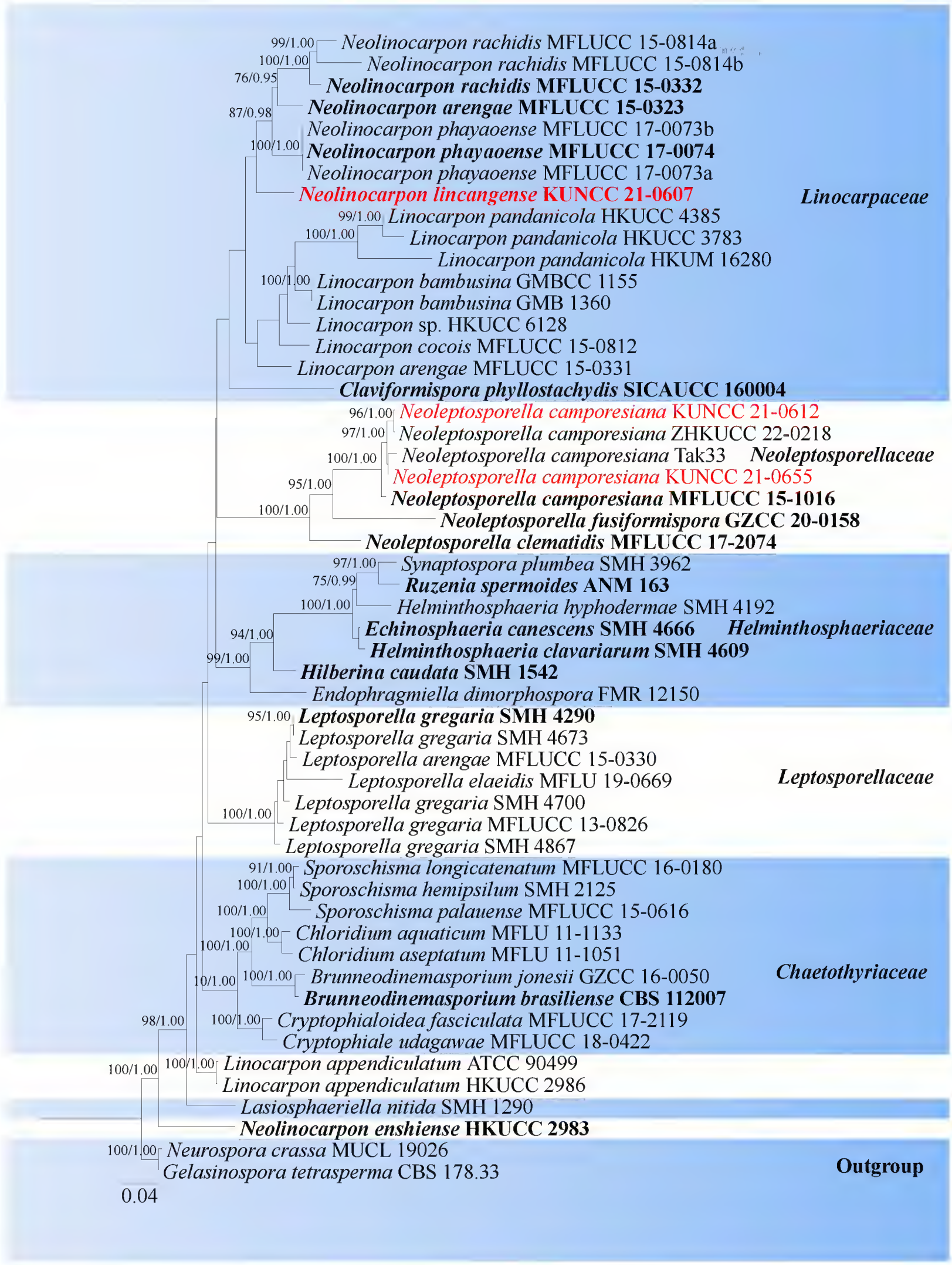
99/1.00 Neolinocarpon rachidis MFLUCC 15-0814a
100/1.00 Neolinocarpon rachidis MFLUCC 15-0814b
76/0.95 Neolinocarpon rachidis MFLUCC 15-0332
87/0.98 Neolinocarpon arengae MFLUCC 15-0323
Neolinocarpon phayaoense MFLUCC 17-0073b
100/1.00 Neolinocarpon phayaoense MFLUCC 17-0074
Neolinocarpon phayaoense MFLUCC 17-0073a
Neolinocarpon lincangense KUNCC 21-0607
Linocarpaceae
99/1.00 Linocarpon pandanicola HKUCC 4385
100/1.00 Linocarpon pandanicola HKUCC 3783
Linocarpon pandanicola HKUM 16280
100/1.00 Linocarpon bambusina GMBCC 1155
Linocarpon bambusina GMB 1360
Linocarpon sp. HKUCC 6128
Linocarpon cocois MFLUCC 15-0812
Linocarpon arengae MFLUCC 15-0331
Claviformispora phyllostachydis SICAUCC 160004
96/1.00 Neoleptosporella camporesiana KUNCC 21-0612
97/1.00 Neoleptosporella camporesiana ZHKUCC 22-0218
100/1.00 Neoleptosporella camporesiana Tak33
Neoleptosporellaceae
Neoleptosporella camporesiana KUNCC 21-0655
95/1.00 Neoleptosporella camporesiana MFLUCC 15-1016
100/1.00 Neoleptosporella fusiformispora GZCC 20-0158
Neoleptosporella clematidis MFLUCC 17-2074
97/1.00 Synaptospora plumbea SMH 3962
75/0.99 Ruzenia spermoides ANM 163
100/1.00 Helminthosphaeria hyphodermae SMH 4192
Echinosphaeria canescens SMH 4666
Helminthosphaeriaceae
94/1.00 Helminthosphaeria clavariarum SMH 4609
99/1.00 Hilberina caudata SMH 1542
Endophragmiella dimorphospora FMR 12150
95/1.00 Leptosporella gregaria SMH 4290
Leptosporella gregaria SMH 4673
Leptosporella arengae MFLUCC 15-0330
Leptosporella elaeidis MFLU 19-0669
Leptosporellaceae
Leptosporella gregaria SMH 4700
100/1.00 Leptosporella gregaria MFLUCC 13-0826
Leptosporella gregaria SMH 4867
91/1.00 Sporoschisma longicatenatum MFLUCC 16-0180
100/1.00 Sporoschisma hemipsilum SMH 2125
100/1.00 Sporoschisma palauense MFLUCC 15-0616
100/1.00 Chloridium aquaticum MFLU 11-1133
100/1.00 Chloridium aseptatum MFLU 11-1051
10/1.00 100/1.00 Brunneodinemasporium jonesii GZCC 16-0050
Brunneodinemasporium brasiliense CBS 112007
Chaetothyriaceae
98/1.00 100/1.00 Cryptophialoidea fasciculata MFLUCC 17-2119
Cryptophiale udagawae MFLUCC 18-0422
100/1.00 100/1.00 Linocarpon appendiculatum ATCC 90499
Linocarpon appendiculatum HKUCC 2986
Lasiosphaeriella nitida SMH 1290
Neolinocarpon enshiense HKUCC 2983
100/1.00 Neurospora crassa MUCL 19026
Gelasinospora tetrasperma CBS 178.33
Outgroup
0.04

Figure 7. Phylogram generated from ML analysis based on LSU, ITS, ACT, *tef*1-α and TUB sequence data representing Chaetothyriaceae, Helminthosphaeriaceae, Leptosporellaceae, Linocarpaceae and Neoleptosporellaceae. Related sequences are obtained following Zhang et al. (2023c), Luo et al. (2025) and Habib et al. (2025). Forty-six strains are included in the combined analyses, which comprise 2630 characters for SSU, LSU, ITS, and *tef*1-α alignment. *Gelasinospora tetrasperma* (CBS 178.33) and *Neurospora crassa* (MUCL 19026) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -20236.771109 is presented. The matrix had 812 distinct alignment patterns, with 48.23% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.232490, C = 0.268062, G = 0.305807, T = 0.193641; substitution rates AC = 1.013194, AG = 1.913555, AT = 0.940548, CG = 1.191676, CT = 5.116146, GT = 1.0000. Gamma distribution shape parameter α = 0.317721 and tree-length = 2.260989. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and posterior probability values greater than 0.95 from BYPP analysis labelled on the nodes. Strains of the newly described species are in red, while type strains are in bold.

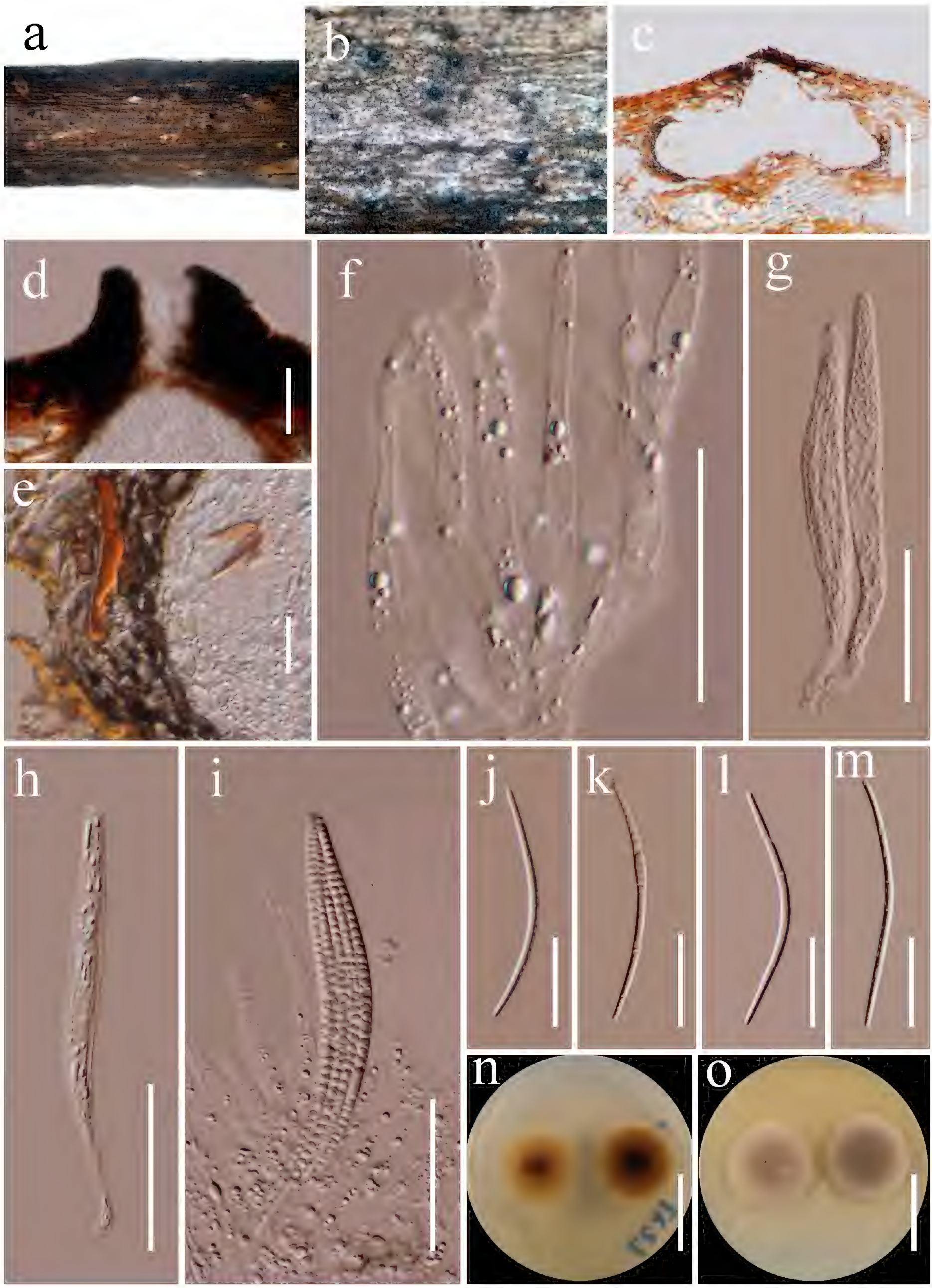

Figure 8. *Neolinocarpon lincangense* (HKAS 122751, holotype). **a, b.** Appearance of ascomata on host substrate; **c.** Section of ascoma; **d.** Section of ostiole; **e.** Peridium; **f.** Hamathecium; **g–i.** Asci; **j–m.** Ascospores; **n, o.** Culture characters on PDA (**o** from above; **n** from below). Scale bars: 200 μm (**c, e**); 50 μm (**d**); 30 μm (**f, g–i**); 40 μm (**j–m**); 30 mm (**n, o**).

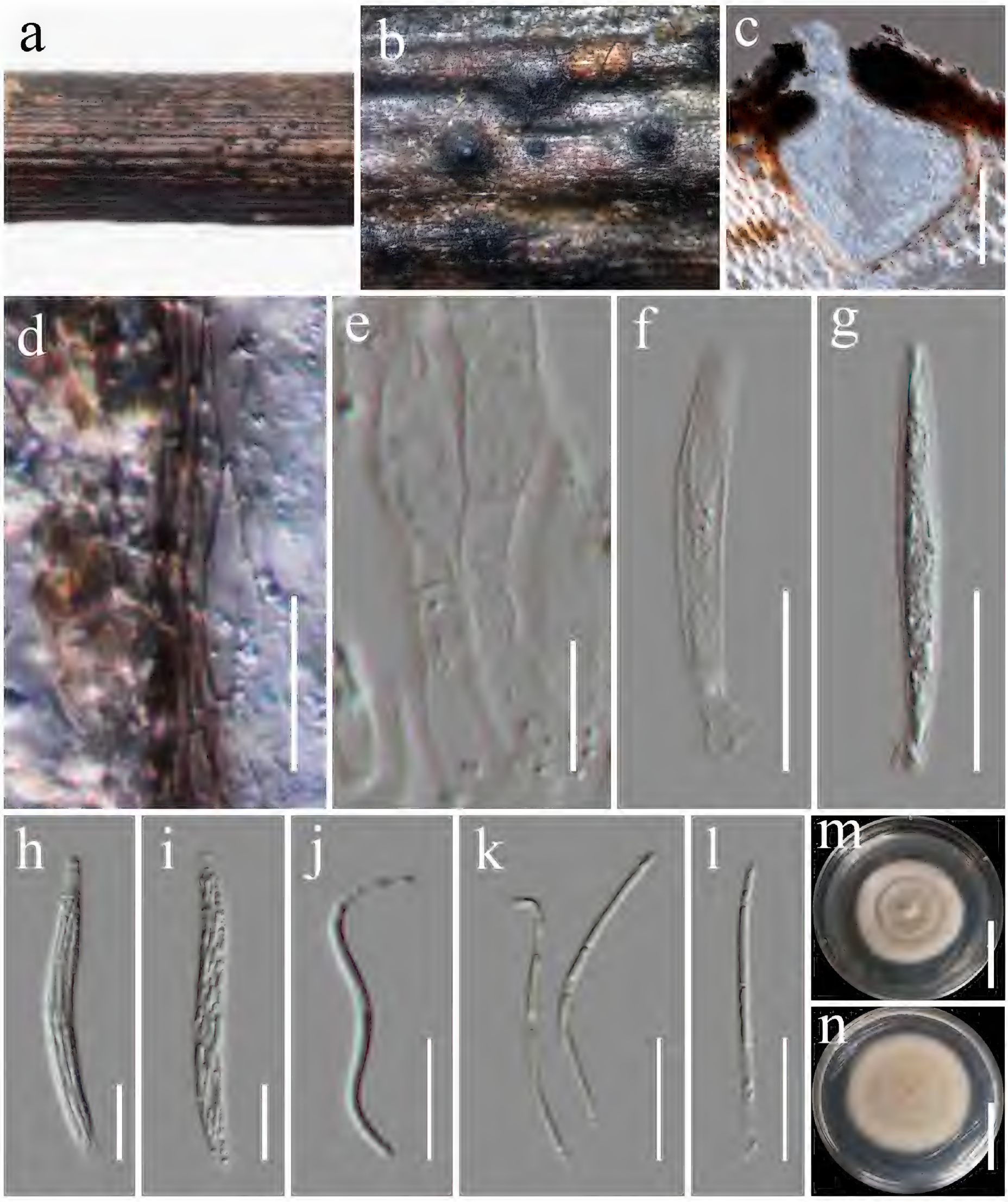

Figure 9. *Neoleptosporella camporesiana* (HKAS 122885). **a, b.** Appearance of ascomata on host substrate; **c.** Section of ascoma; **d.** Peridium; **e.** Pseudoparaphyses; **f–i.** Asci; **j–l.** Ascospores; **m, n.** Culture characters on PDA (**m** from above; **n** from below). Scale bars: 100 µm (**c**); 20 µm (**d**); 10 µm (**e**); 20 µm (**f–l**); 20 mm (**m, n**).

J- apical ring and filiform ascospores (Hyde et al. 2020a). Sequence comparison for the ITS and *tef*1-α region between our isolates (KUNCC 21-0612, KUNCC 21-0655) and *Neoleptosporella camporesiana* (MFLUCC 15-1016) showed no significant base pair differences. Therefore, we identified our taxon as a new host record of *Neoleptosporella camporesiana* from *Castanopsis mekongensis* (Fagaceae) and *Sorbus rehderiana* (Rosaceae) in China.

Planisphaeriales J.F. Zhang, Jian K. Liu & K.D. Hyde, 2023

Planisphaeriaceae J.F. Zhang, Jian K. Liu & K.D. Hyde, Fungal Diversity 222: 114 (2023)

Notes. Planisphaeriaceae was established by Zhang et al. (2023b) to accommodate the genus *Planisphaeria*, with *Planisphaeria reniformispora* designated as the type species. The family was delineated based on morphological characteristics and phylogenetic analyses using LSU, SSU, *tef*1-α, and *rpb*2 sequence data from species within Sordariomycetes. Currently, Planisphaeriaceae comprises a single genus, *Planisphaeria*, which includes two species, *P. reniformispora* and *P. karsti*. Members of this family are saprophytic and occur on dead woody plants (Zhang et al. 2023b; Hyde et al. 2024b). In this study, we introduced two new host records, *Planisphaeria karsti* and *P. reniformispora* from *Trigonobalanus doichangensis* (Fagaceae).

***Planisphaeria karsti* J.F. Zhang & K.D. Hyde, Fungal Diversity 222: 117 (2023)**
Index Fungorum: IF900742
Facesoffungi Number: FoF14598
Fig. 11

Description. ***Saprobic*** on dead woody twigs. **Sexual morph:** ***Ascomata*** 300–400 μm high, 220–250 μm diam. ($\bar{x}$ = 345 × 240 μm, n = 5), immersed to erumpent, solitary or scattered, subglobose to globose, fattened at the base, glabrous, black, coriaceous. ***Ostiole*** central, 105–160 μm long, 50–75 μm diam. ($\bar{x}$ = 138 × 63 μm, n = 5), immersed, long papillate, hyaline hyphae with periphyses. ***Peridium*** 10–14 μm wide, composed of dark brown, thick-walled cells of ***textura angularis*** that fused with host tissues. ***Hamathecium*** 2.5–4.5 μm wide, comprising abundant, branched, septate, hyphae like paraphyses, anastomosed. ***Asci*** 80–110 × 23–30 μm ($\bar{x}$ = 94 × 27 μm, n = 20), 8-spored, unitunicate, broadly clavate, short pedicellate, rounded to truncate at the apex, with an inconspicuous apical ring. ***Ascospores*** 22–27 × 7–10 μm ($\bar{x}$ = 24 × 8 μm, n = 30), overlapping, biseriate, hyaline, reniform to allantoid, aseptate, rounded at both ends, curved, guttulate, verrucose, without mucilaginous sheath or appendages. **Asexual morph:** Undetermined.

Culture characteristics. Ascospores germinated on PDA within 24 h at room temperature (25 °C). Colonies on PDA, reaching 20 mm diameter after one week at 20–25 °C, mycelia superficial, irregular, flat, fimbriate, undulate, white; reverse, white, sometimes yellowish at the center.

Material examined. China • Yunnan Province, Lancang, (24°5'30"N, 100°5'33"E, elevation: 1557.49 m), on dead woody twigs of *Trigonobalanus doichangensis* (Fagaceae), 19 July 2020, G.C. Ren, GY02 (HKAS 122721), living culture KUNCC 21-0543.

GenBank numbers. ITS: PX568863, LSU: PX473155, SSU: PX583844, *tef*1-α: PX521735, *rpb*2: PX521739.

Known hosts and distribution. China, on dead branch of woody plant (Zhang et al. 2023b), on dead woody twigs of *Trigonobalanus doichangensis* (Fagaceae) (this study).

Notes. According to the multi-gene phylogenetic analyses of combined LSU, SSU, ITS, *tef*1-α, and *rpb*2 sequence dataset, our new isolate (KUNCC 21-0543) nested with *Planisphaeria karsti* (GZAAS 20-4008), which was isolated from dead branch of woody plant in China (Zhang et al. 2023b) with 87% ML bootstrap support (Fig. 10). The new collection shares similar morphology with the type material of *Planisphaeria karsti* in having subglobose to globose, fattened as the base, black ascostromata, periphyses ostiole, broadly clavate asci with short pedicellate and an inconspicuous apical ring, hyaline, one-celled, aseptate, guttulate, verrucose ascospores. However, there is a difference in the shape of the spores, *Planisphaeria karsti* has irregular ellipsoid ascospores tapered towards one end and rounded at another end, whereas the new collection has reniform to allantoid ascospores with rounded ends. Sequence comparison for the LSU and SSU region between our isolates (KUNCC 21-0543) and *P. karsti* (GZAAS 20-4008) showed no significant base pair differences, 1.1% (11/ 1037 bp, without gaps) base pair difference for *rpb*2 region, but we were unable to compare ITS and *tef*1-α gene of *P. karsti* as there was no sequence data. We report our collection as a new host record of *P. karsti* from *Trigonobalanus doichangensis* (Fagaceae) in China.

Planisphaeria reniformispora **J.F. Zhang & K.D. Hyde, Fungal Diversity 222: 117 (2023)**

Index Fungorum: IF900741

Facesoffungi Number: FoF14597

Fig. 12

Description. ***Saprobic*** on dead woody twigs. **Sexual morph:** ***Ascomata*** 300–380 μm high, 200–370 μm diam. ($\bar{x}$ = 340 × 280 μm, n = 5), immersed to erumpent, solitary or scattered, uni-loculate, subglobose to obpyriform, fattened at the base, black, coriaceous, central ostiole. ***Peridium*** 13–20 μm wide, composed of brown, thick-walled cells of ***textura angularis*** that merge with host tissue. ***Hamathecium*** 3–6 μm wide, comprising abundant, branched, septate, hyphae-like paraphyses, anastomosed. ***Asci*** 60–87 × 16–24 μm ($\bar{x}$ = 72 × 20 μm, n = 20), 8-spored, unitunicate, clavate to broadly clavate, with a short pedicel, rounded to truncate at the apex, with an inconspicuous apical ring. ***Ascospores*** 19–23 × 8–10 μm ($\bar{x}$ = 21 × 9 μm, n = 30), overlapping biseriate, hyaline, mostly irregular ovoid, straight, tapered towards one end and rounded at other end, aseptate, thick-walled, guttulate, verrucose, without mucilaginous sheath or appendages. **Asexual morph:** Undetermined.

Culture characteristics. Ascospores germinated on PDA within 24 h at room temperature (25 °C). Colonies on PDA, reaching 50 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, sparse mycelia, flat, fimbriate, white; reverse, dark brown.

Material examined. China • Yunnan Province, Lancang, (24°5'30"N, 100°5'33"E, elevation: 1557.49 m), on dead woody twigs of *Trigonobalanus doichangensis* (Fagaceae), 19 July 2020, G.C. Ren, GY42 (HKAS 122722), living culture KUNCC 21-0568.

GenBank numbers. ITS: PX568864, LSU: PX473156, SSU: PX583845, *tef*1-α: PX521736.

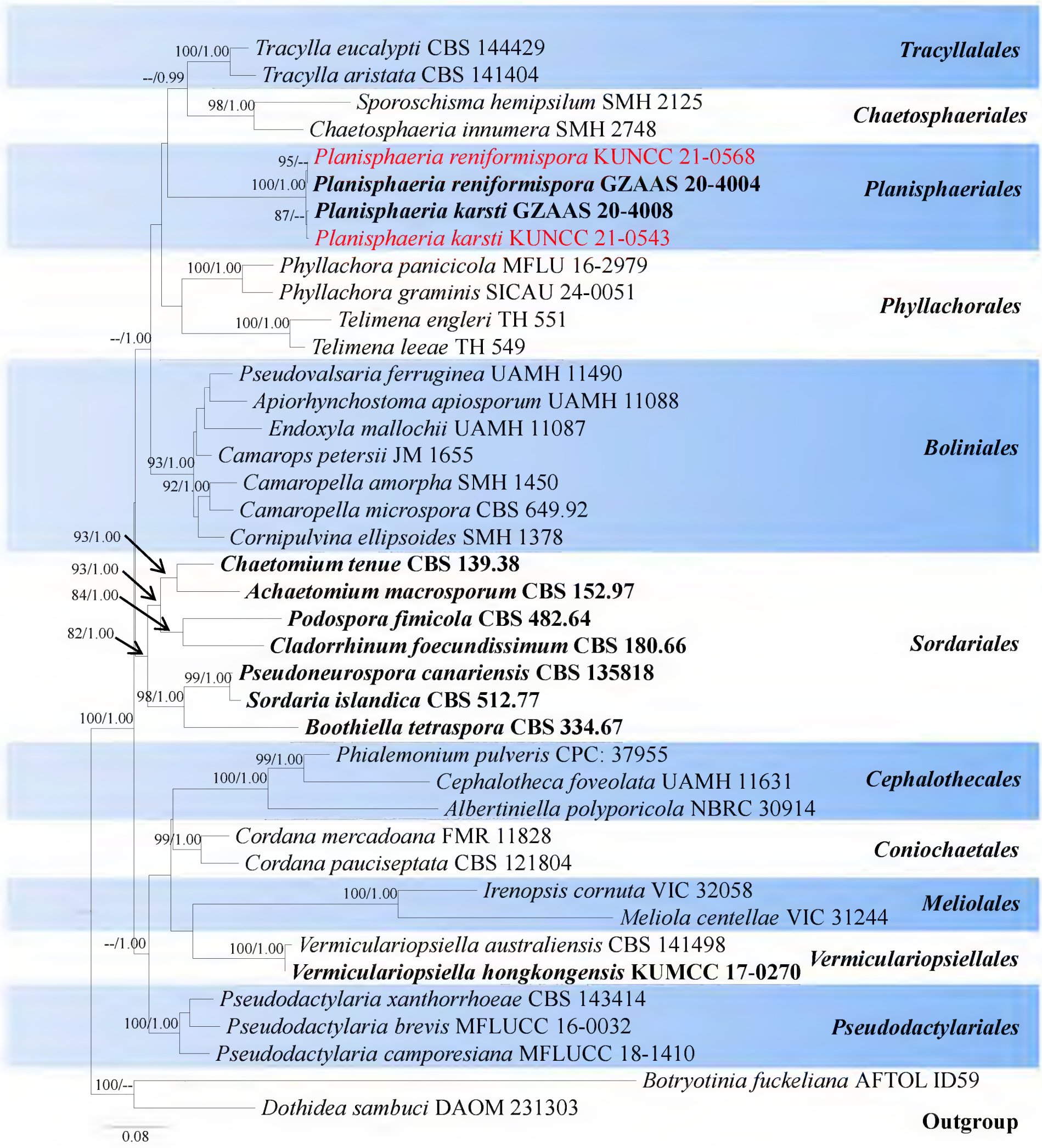

Figure 10. Phylogram generated from ML analysis based on LSU, SSU, ITS, *tef*1-α and *rpb*2 sequence data representing Sordariomycetes. Related sequences are obtained following Zhang et al. (2023b). Forty strains are included in the combined analyses, which comprise 4105 characters for LSU, SSU, ITS, *tef*1-α and *rpb*2 alignment. *Botryosphaeria fuckeliana* (AFTOLID59) and *Dothidea sambuci* (DAOM 231303) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -28303.773266 is presented. The matrix had 1766 distinct alignment patterns, with 54.76% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.243984, C = 0.250047, G = 0.288655, T = 0.217314; substitution rates AC = 1.401636, AG = 2.371260, AT = 1.506416, CG = 1.236045, CT = 6.334641, GT = 1.0000. Gamma distribution shape parameter α = 0.355387 and tree-length = 4.905723. The Bayesian analysis calculated the average standard deviation of split frequencies at the end of 2,000,000 MCMC generations as 0.006199. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and posterior probability values greater than 0.95 from BYPP analysis labelled on the nodes. Strains of the newly described species are in red, while type strains are in bold.

Figure 11. *Planisphaeria karsti* (HKAS 122721). **a, b.** Appearance of ascomata on host substrate; **c.** Section of ascoma; **d.** Section of ostiole; **e.** Peridium; **f.** Paraphyses; **g–k.** Asci; **l–o.** Ascospores; **p.** A germinating ascospore; **q, r.** Culture characters on PDA (**q** from above; **r** from below). Scale bars: 100 μm (**c, d**); 50 μm (**e**); 20 μm (**f**); 50 μm (**g–k**); 10 μm (**l–p**); 20 mm (**q, r**).

Known hosts and distribution. China, on dead branch of unidentified woody plant (Zhang et al. 2023b); on dead woody twigs of *Trigonobalanus doichangensis* (Fagaceae) (this study).

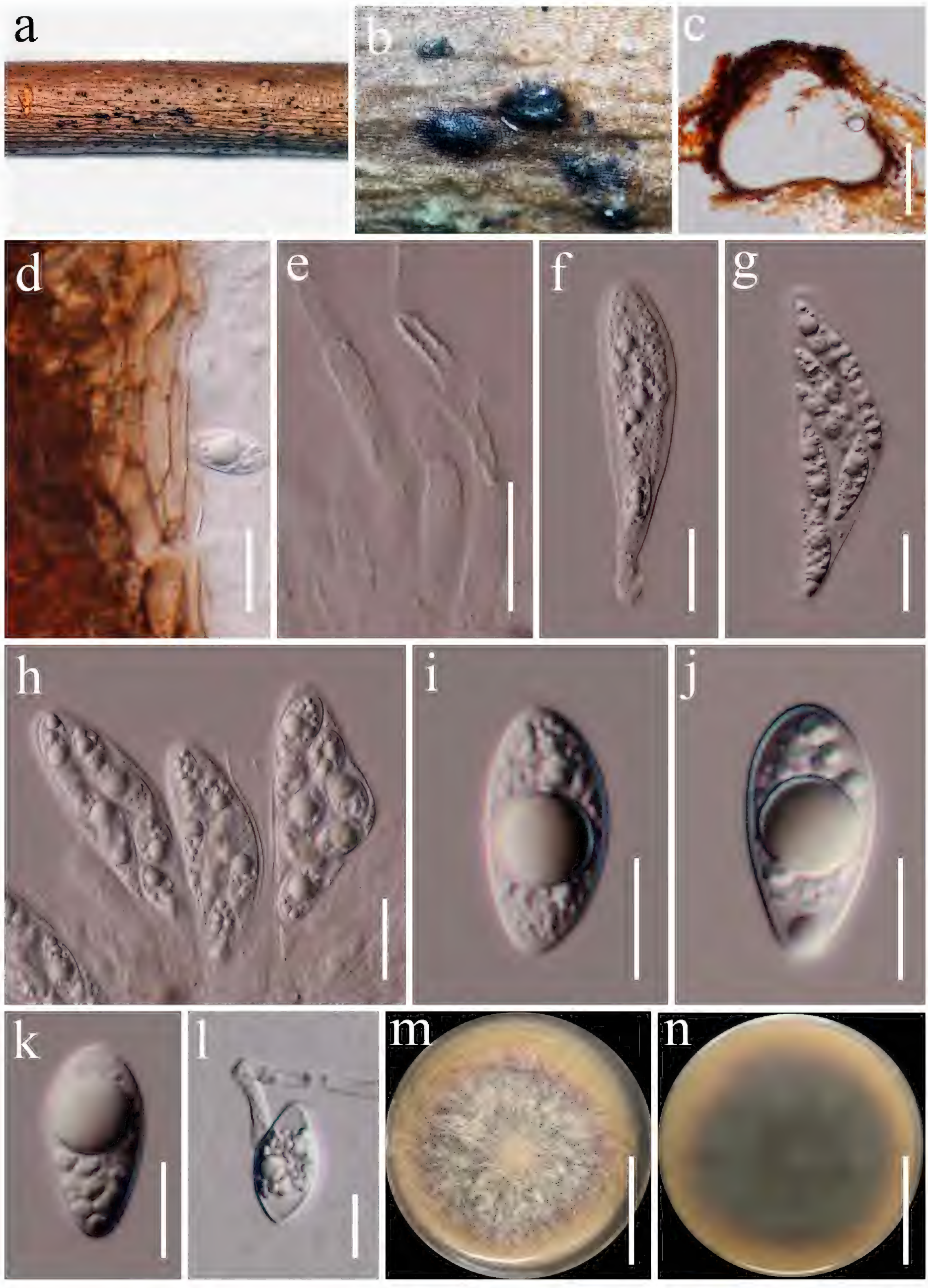

Figure 12. *Planisphaeria reniformispora* (HKAS 122722). **a, b.** Appearance of ascomata on host substrate; **c.** Section of ascoma; **d.** Peridium; **e.** Paraphyses; **f–h.** Asci; **i–k.** Ascospores; **l.** A germinating ascospore; **m, n.** Culture characters on PDA (**m** from above; **n** from below). Scale bars: 150 μm (**c**), 20 μm (**d–h**), 10 μm (**i–l**), 20 mm (**m, n**).

Notes. According to the multi-gene phylogenetic analyses of combined LSU, SSU, ITS, *tef*1-α, and *rpb*2 sequence dataset, our new isolate (KUNCC 21-0568) nested with *Planisphaeria reniformispora* (GZAAS 20-4004), which was isolated from dead branch of woody plant in China (Zhang et al. 2023b) with 95% ML bootstrap support (Fig. 10). The new collection shares similar morphology with the type material of *Planisphaeria reniformispora* in having immersed to erumpent, subglobose to obpyriform, fattened at the base, black ascomata, clavate asci and hyaline, one-celled, guttulate, verrucose ascospores. However, there is a difference in the shape of the spores, *Planisphaeria reniformispora* in having reniform ascospores, whereas the new collection has irregular ovoid ascospores. Sequence comparison for the LSU and SSU region between our isolates (KUNCC 21-0568) and *P. reniformispora* (GZAAS 20-4004) showed no significant base pair differences. Therefore, we identified our taxon as a new host record of *P. reniformispora* from *Trigonobalanus doichangensis* (Fagaceae) in China.

Sordariales Chadef. ex D. Hawksw. & O.E. Erikss., 1986

Lasiosphaeridaceae S.K. Huang, Maharachch. & K.D. Hyde, Fungal Diversity, 111: 443–572 (2021).

Notes. Lasiosphaeridaceae was established by Huang et al. (2021) in Sordariales to accommodate the monotypic genus *Lasiosphaeris*, based on both morphological characteristics and multigene phylogenetic analyses of LSU, ITS, TUB and *rpb*2 sequence data. Currently, the genus comprises four species, *L. arenicola* (=*Cercophora arenicola*), *L. hispida* and *L. hirsuta* and *L. indica* (Huang et al. 2021). In this study we introduced a new host record of *Lasiosphaeris hispida*.

***Lasiosphaeris hispida* (Tode) Clem., Gen. fung. (Minneapolis): [173] (1909)**
Index Fungorum: IF531338
Facesoffungi Number: FoF10021
Fig. 14

Basionym. *Sphaeria hispida* Tode, Fung. mecklenb. sel. (Lüneburg) 2: 17 (1791)

Description. ***Saprobic*** on dead woody twigs. **Sexual morph:** ***Ascomata*** 380–460 µm high, 350–460 µm diam. ($\bar{x}$ = 420 × 400 µm, n = 5), perithecial, solitary, superficial to semi-immersed, globose to subglobose, black, ostiolate, coriaceous, with numerous, septate, brown, setae (4–5 diam.). ***Peridium*** 40–56 µm ($\bar{x}$ = 50 µm, n = 30) wide, comprising two layers, outer layer composed of brown cells of ***textura angularis*** to ***textura prismatica***, inner layer composed of hyaline cells of ***textura angularis***. ***Paraphyses*** 3–5 µm wide, numerous, hyaline, filiform, septate, branched, slightly constricted at the septa, embedded in a gelatinous matrix. ***Asci*** 210–270 × 12–18 µm ($\bar{x}$ = 250 × 15 µm, n = 20), 8-spored, unitunicate, cylindrical to clavate, long pedicellate, apex rounded, with apical globule, apical ring distinct. ***Ascospores*** 70–76 × 5.5–8 µm ($\bar{x}$ = 73 × 6.7 µm, n = 30), bi-seriate, cylindrical, slightly curved near the base, hyaline and aseptate when young, becoming pale brown and 7-septate when mature, rounded at the apex, pointed at the base, guttule, smooth-walled. **Asexual morph:** Undetermined.

Culture characteristics. Ascospores germinating on PDA within 24 h at room temperature (25 °C). Colonies on PDA, reaching 30–40 mm diameter after one week at 20–25 °C, mycelia superficial, irregular, flat, fimbriate, undulate entire, grey to atrovirens; reverse, atrovirens.

Material examined. China • Yunnan Province, Nixi Diqing, Xianggelila, Nixi, (27°25'37"N, 99°50'45"E, elevation: 3090 m), on dead woody twigs of *Rhododendron rubiginosum* (Ericaceae), 1 September 2020, G.C. Ren, NX24 (HKAS 122766), living culture KUNCC 21-0645.

GenBank numbers. ITS: PX568865, LSU: PX473157, SSU: PX583846.

Known hosts and distribution. On dead wood in Germany (type locality) and USA (Fuckel 1870; Miller and Huhndorf 2005), on dead woody twigs of *Rhododendron rubiginosum* (Ericaceae) in China (this study).

Notes. Multi-loci phylogenetic analyses based on a concatenated LSU, ITS, and TUB sequence dataset show that our new collections (KUNCC 21-0645) clusters with *Lasiosphaeris hispida* (CBS95572, SMH3336) with 100% ML and 1.00 BYPP bootstrap support (Fig. 13). Sequence comparison for the ITS, LSU and TUB region between our isolates (KUNCC 21-0645) and *Lasiosphaeris hispida* (SMH3336) showed no significant base pair differences. Our collection (KUNCC 21-0645) resembles *Lasiosphaeris hispida* in having sporodochial conidiomata; septate, subhyaline to light brown mycelium; mononematous, cylindrical, light brown conidiophores; monoblastic, terminal, light brown conidiogenous cells and muriform, oval to long elliptical conidia often with a hyaline, elliptical to globose, 0–multiple-basal cell (Huang et al. 2021). Therefore, we introduce our collection as the first record of *L. hispida* from *Rhododendron rubiginosum* (Ericaceae), and first time reported in China.

Xylariales Nannf., Nova Acta R. Soc. Scient. upsal., Ser. 4 8(no. 2): 66 (1932)

Barrmaeliaceae Voglmayr & Jaklitsch, Mycol. Progr. 17(1–2): 162 (2018)

Notes. Barrmaeliaceae is recently established by Voglmayr et al. (2018) based on multigene phylogenetic analyses using ITS, LSU, *rpb*2, and TUB sequences. The family was created to accommodate the type genus *Barrmaelia* and *Entosordaria*. Hyde et al. (2024b) proposed that *Induratia*, previously placed in the family Induratiaceae (Samarakoon et al. 2020), should be accommodated in Barrmaeliaceae due to its closer phylogenetic affinity with this family. In this study we introduced a new species *Barrmaelia nixiensis*.

***Barrmaelia nixiensis* G.C Ren & Wanas., sp. nov.**

Index Fungorum: IF904526

Facesoffungi Number: FoF18854

Fig. 16

Etymology. The specific epithet "*nixiensis*" reflects nixi where the holotype was collected.

Holotype. HKAS 122884

Description. ***Saprobic*** on dead woody twigs. **Sexual morph:** ***Ascomata*** 450–600 µm high, 450–530 µm diam. ($\bar{x}$ = 520 × 490 µm, n = 5), immersed in bark, soli-

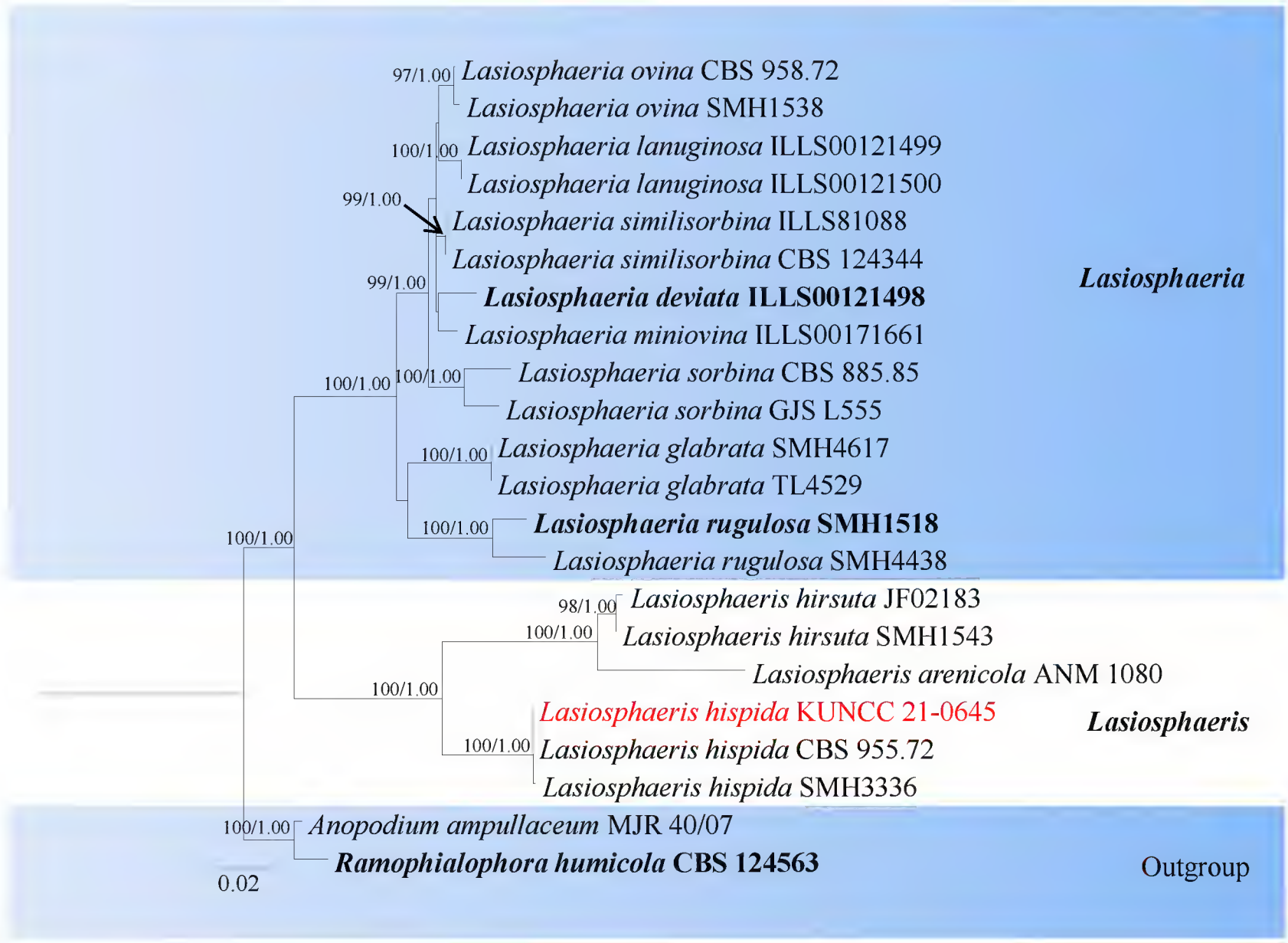

Figure 13. Phylogram generated from ML analysis based on LSU, ITS, and TUB sequence data representing *Lasiosphaeria* and *Lasiosphaeris*. Related sequences are obtained following Huang et al. (2021). Twenty-two strains are included in the combined analyses, which comprise 2669 characters for LSU, ITS and TUB alignment. *Anopodium ampullaceum* (MJR 40/07) and *Ramophialophora humicola* (CBS 124563) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -8642.701866 is presented. The matrix had 545 distinct alignment patterns, with 26.27% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.230199, C = 0.259303, G = 0.278833, T = 0.231665; substitution rates AC = 1.180009, AG = 2.589188, AT = 1.230892, CG = 1.493571, CT = 9.951940, GT = 1.0000. Gamma distribution shape parameter α = 0.134824 and tree-length = 0.536057. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and posterior probability values greater than 0.95 from BYPP analysis labelled on the nodes. Strains of the newly described species are in red, while type strains are in bold.

tary or aggregated, globose to subglobose, uni-loculate, coriaceous, visible as black dots, ostiolar openings on the stromatal surface. ***Ostioles*** centric, often elongate, ostiolar pore rounded, shiny and slightly raised. ***Peridium*** 12–18 µm thick, composed of brown cells of ***textura angularis***, thick–walled. ***Paraphyses*** 2.5–4 µm wide, abundant, hyaline, filamentous, sinuous, unbranched, septate, guttulate, slightly tapering towards the apex, obtuse. ***Asci*** 75–95 × 5–6 µm ($\bar{x}$ = 90 × 5.7 µm, n = 20), 8-spored, unitunicate, cylindrical, straight or curved, long pedicellate, apically rounded. ***Ascospores*** 8.5–11 × 3.2–4 µm ($\bar{x}$ = 9.8 × 3.7 µm, n = 30), uniseriate, unicellular, ellipsoidal to oblong, straight, brown, small guttules, smooth-walled, without a gelatinous sheath and without germ slit. **Asexual morph:** Undetermined.

Culture characteristics. Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes are produced from the basal and apical cell of ascospore. Colonies on PDA, reaching 20 mm diameter after one week at 20–25 °C, mycelia superficial, raised, circular, fimbriate, dense, flat, entire edge, white to light brown; reverse, light brown at the edge, dark brown at the center.

Material examined. China • Yunnan Province, Diqing, Xianggelila, Nixi, (27°25'37"N, 99°50'45"E, elevation: 3090 m), on dead woody twigs of

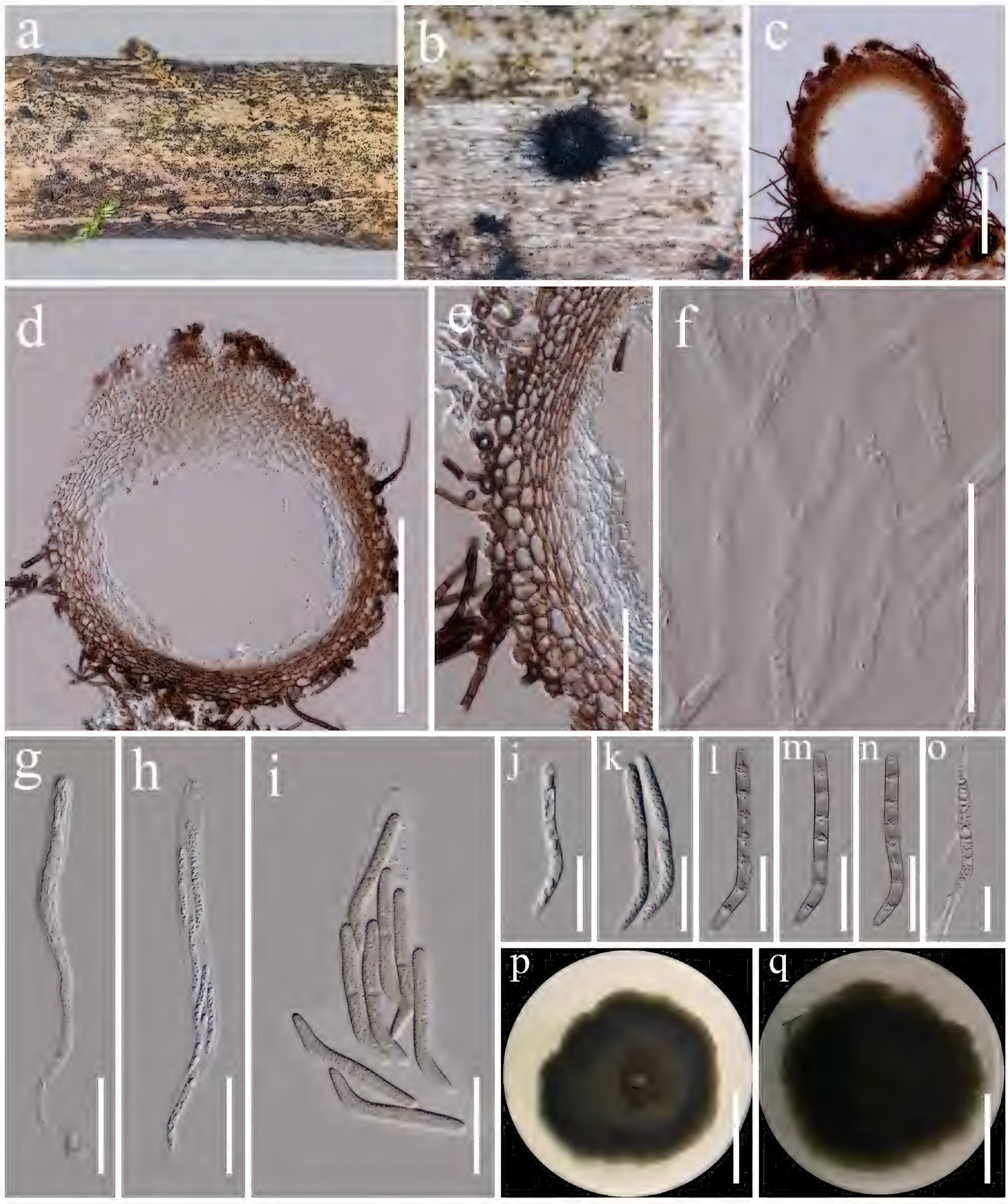

Figure 14. *Lasiosphaeris hispida* (HKAS 122766). **a, b.** Appearance of ascomata on host surface; **c, d.** Ascoma in cross section; **e.** Peridium; **f.** Paraphyses; **g–i.** Asci; **j–n.** Ascospores; **o.** Germinating ascospore; **p, q.** Culture characters on PDA (**p** from above; **q** from below). Scale bars: 200 μm (**c, d**); 50 μm (**e, f–i**); 30 μm (**j–o**); 20 mm (**p, q**).

Rhododendron rubiginosum (Ericaceae), 31 August 2020, G.C. Ren, NX17 (holotype, HKAS 122884), ex-type culture KUNCC 21-0642.

GenBank numbers. ITS: PP663076, LSU: PP663082, *tef*1-α: PX521737.

Notes. Multi-loci phylogenetic analyses based on a concatenated LSU, ITS, *tef*1-a and *rpb*2 dataset show that our new collections (KUNCC 21-0642) clus-

ters with *Barrmaelia macrospora* (CBS 142768), but they did not receive statistical support values (Fig. 15). Sequence comparison for the ITS region between *Barrmaelia nixiensis* (KUNCC 21-0642) and *Barrmaelia macrospora* (CBS 142768) showed a 1.86% (10/ 538 bp, without gaps) base pair difference, 2% (15/ 751 bp, without gaps) base pair difference for *tef*1-a region. Morphologically, *Barrmaelia nixiensis* differs from *B. macrospora* in having comparatively smaller asci (75–95 × 5–6 vs. 108–143 × 9–11) with long pedicellate, smaller asci ascospores (8.5–11 × 3.2–4 vs. (18.2–)20.5–24.0(–26.0) × (4.0–)4.8–5.9(–6.5)), while *B. macrospora* has larger asci with short stipe and larger ascospores with a lighter coloured band at the concave side and germ slit (Voglmayr et al. 2018). Based on morphology and the phylogenetic distinctiveness, we introduce *Barrmaelia nixiensis* as a new species.

Graphostromataceae M.E. Barr, J.D. Rogers & Y.M. Ju, Mycotaxon 48: 533 (1993)

Notes. Graphostromataceae was introduced by Barr et al. (1993), which includes saprobes, endophytes and pathogens on numerous plant species globally (Chen et al. 2024). Currently, five genera are recognized within the family, Biscogniauxia, Camillea, Graphostroma, Obolarina and Vivantia (Hyde et al. 2024b). In this study, we introduced a new species, *Biscogniauxia xishuangbannaensis*.

***Biscogniauxia xishuangbannaensis* G.C Ren & Wanas., sp. nov.**

Index Fungorum: IF904527

Facesoffungi Number: FoF18855

Fig. 17

Etymology. The specific epithet "*xishuangbannaensis*" reflects xishuangbanna where the holotype was collected.

Holotype. HKAS 122774.

Description. ***Saprobic*** on dead woody twigs. **Sexual morph:** ***Stromata*** 3–18 × 2–7 mm, superficial, aggregated, applanate, cover the wood surface, dull brown to black, carbonaceous, visible as black dots on the stromata. ***Ascomata*** 300–480 × 250–400 µm ($\bar{x}$ = 360 × 315 µm, n = 5), ovoid to obpyriform, laterally compressed. ***Ostioles*** pointed, raised. ***Paraphyses*** 3–7 µm wide, long, numerous, filamentous, flexuous, septate, constricted at the septa, apex rounded, slightly tapering towards the apex. ***Asci*** 75–95 × 5.7–9 µm ($\bar{x}$ = 86 × 7.7 µm, n = 20), 8-spored, unitunicate, cylindrical, short pedicellate, with a 5–6.6 × 3.5–5 µm ($\bar{x}$ = 5.8 × 4.2 µm, n = 20), wedge-shaped apical ring, apex rounded. ***Ascospores*** 8–11 × 4.4–6 µm ($\bar{x}$ = 10 × 5 µm, n = 30), uniseriate, unicellular, ellipsoid, rounded ends, hyaline when immature, dark brown to black when mature, 1–2-guttulate, aseptate, with straight germ slit along the entire spore length. **Asexual morph:** Undetermined.

Culture characteristics. Ascospores germinating on PDA within 24 hrs at room temperature. Germ tubes are produced from the basal cells of the ascospore. Colonies on PDA, reaching 55 mm diameter after one week at 20–25 °C, mycelia superficial, circular, dense, fimbriate, entire edged, white; reverse view white.

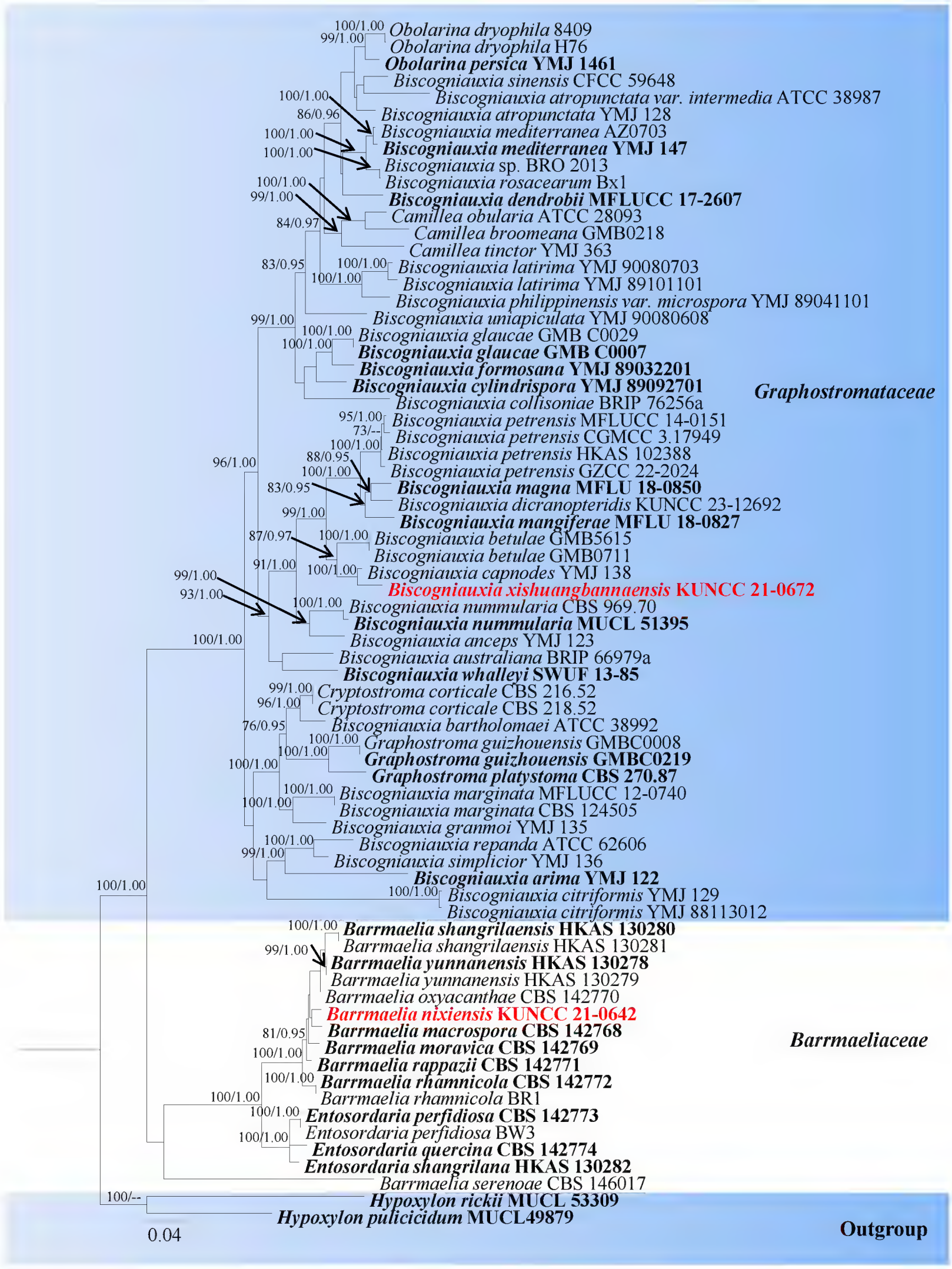

Figure 15. Phylogram generated from ML analysis based on LSU, ITS, *tef*1-α, *rpb*2 and TUB sequence data representing Barrmaeliaceae and Graphostromataceae. Related sequences are obtained following Chen et al. (2024) and GenBank (http://www.ncbi.nlm.nih.gov). Seventy-one strains are included in the combined analyses, which comprise 5409 characters for LSU, ITS, *tef*1-α, *rpb*2 and TUB alignment. *Hypoxylon pulicicidum* (MUCL49879) and *H. rickii* (MUCL 53309). were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -44661.622236 is presented. The matrix had 2258 distinct alignment patterns, with 45.28% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.236549, C = 0.271101, G = 0.252706, T = 0.239644; substitution rates AC = 1.148601, AG = 4.023809, AT = 1.100668, CG = 0.916979, CT = 6.158610, GT = 1.0000. Gamma distribution shape parameter α = 0.244516 and tree-length = 3.234831. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and posterior probability values greater than 0.95 from BYPP analysis labelled on the nodes. Strains of the newly described species are in red, while type strains are in bold.

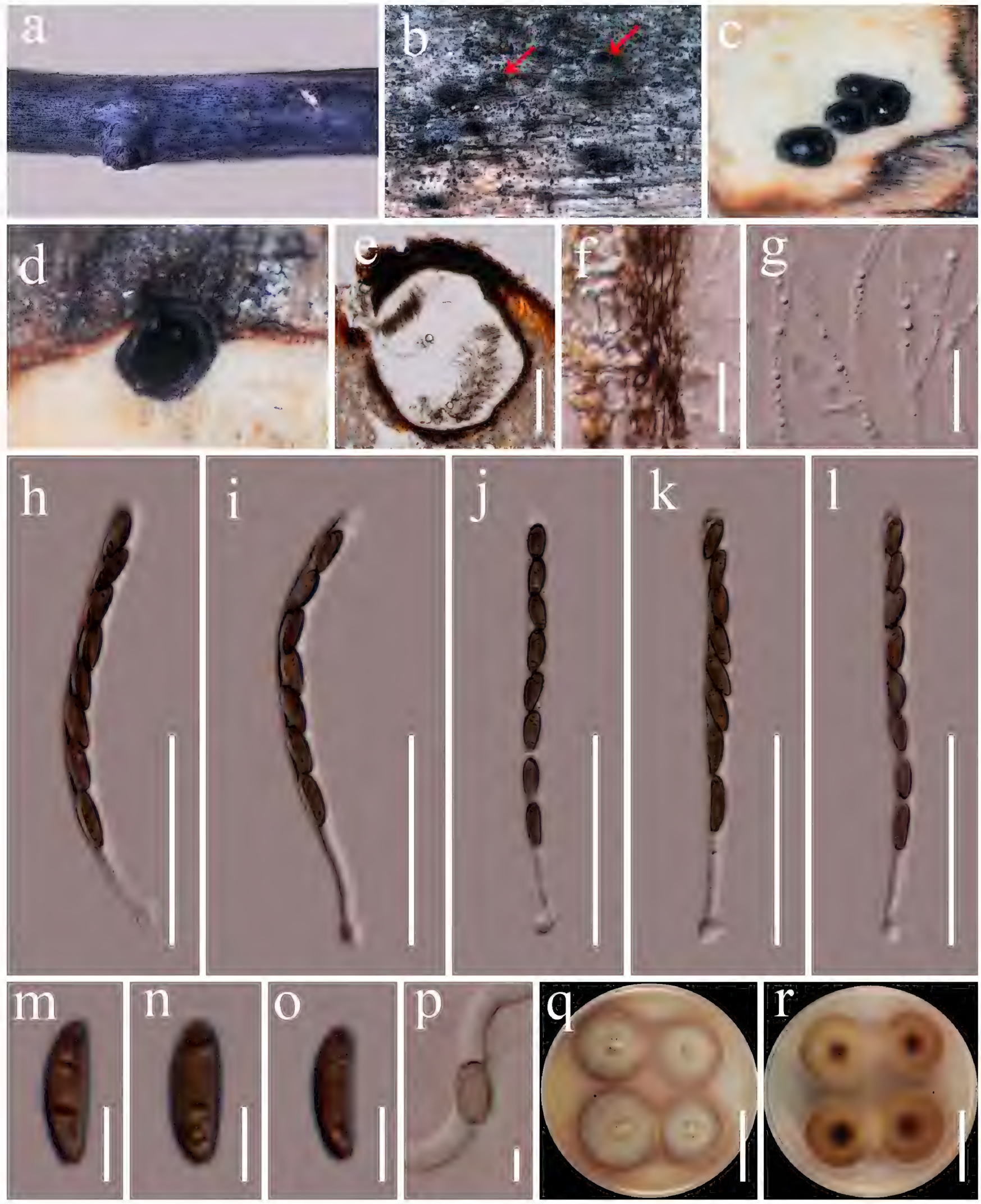

Figure 16. *Barrmaelia nixiensis* (HKAS 122884, holotype). **a, b.** Appearance of ascomata on the host substrate (red arrows indicate ascomata); **c.** Ascomata in transverse section; **d.** Ascoma in vertical section; **e.** Section of the ascoma; **f.** Peridium; **g.** Paraphyses; **h–l.** Asci; **m–o.** Ascospores; **p.** A germinated ascospore; **q, r.** Culture characters on PDA (**q** from above; **r** from below). Scale bars: 200 μm (**e**); 20 μm (**f, g**); 50 μm (**h–l**); 5 μm (**m–p**); 30 mm (**q, r**).

Material examined. CHINA • Yunnan Province, Xishuangbanna, Xishuangbanna Dai Autonomous Prefecture, Jinghong (21°55.19'N, 101°15.24'E, elevation: 522 m), on dead woody twigs of undetermined tree, 15 July 2019, G.C Ren, XS19 (holotype, HKAS 122774), ex-type culture KUNCC 21-0672.

GenBank numbers. ITS: PP663077, LSU: PP663083, SSU: PX583847, *tef*1-α: PX521738, *rpb*2: PX521740.

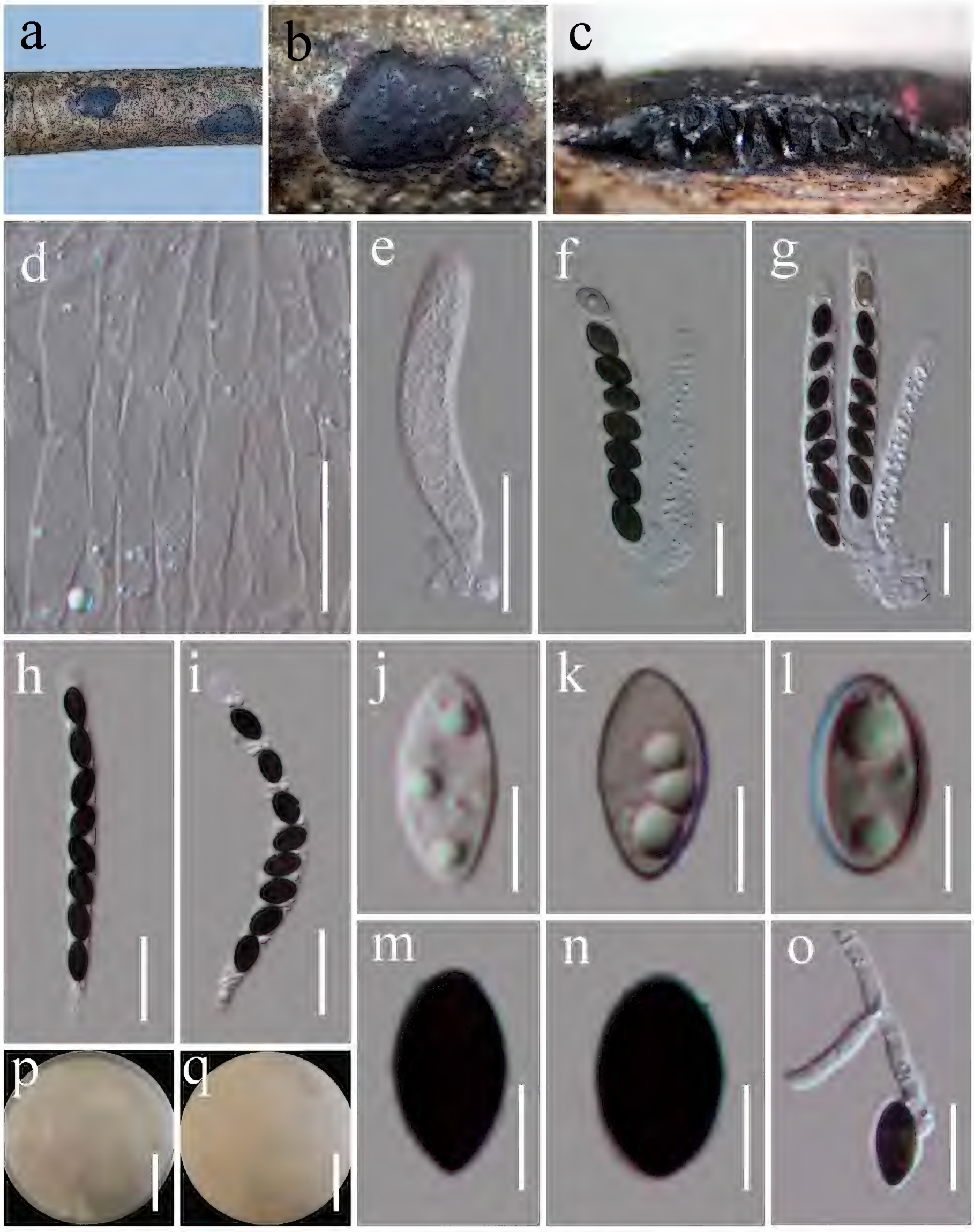

Figure 17. *Biscogniauxia xishuangbannaensis* (HKAS 122774, holotype). **a, b.** Appearance of stromata on the host substrate; **c.** Ascomata in vertical section; **d.** Paraphyses; **e–i.** Asci; **j–n.** Ascospores; **o.** A germinated ascospore; **p, q.** Culture characters on PDA (**p** from above; **q** from below). Scale bars: 20 µm (**d–i**); 5 µm (**j–n**); 10 µm (**o**), 20 mm (**p, q**).

Notes. Multi-loci phylogenetic analyses based on a concatenated LSU, ITS, *tef*1-a, and *rpb*2 dataset show that our new strain (KUNCC 21-0672) clustered with *Biscogniauxia capnodes* (YMJ 138) with 100% ML and 1.00 BYPP bootstrap support (Fig. 15). Sequence comparison for the ITS region between *Biscogniauxia*

xishuangbannaensis (KUNCC 21-0672) and *Biscogniauxia capnodes* (YMJ 138) showed a 2.49% (15/ 602 bp, without gaps) base pair difference, 3.15% (32/ 1015 bp, without gaps) base pair difference for *rpb*2 region. *Biscogniauxia capnodes* differs from our strain by its elongated, erumpent patches, obovoid to tubular perithecia, discoid apical ring and large ascospores (Berkeley 1845; Ju and Rogers 2001). Based on morphology and the phylogenetic distinctiveness, we introduce *Biscogniauxia xishuangbannaensis* as a new species.

Discussion

Over the past few decades, research on fungal diversity in China has expanded substantially (Dai et al. 2015; Wang and Cai 2023). This progress reflects the broad climatic gradients and heterogeneous ecosystems in China, which provide diverse habitats that support high fungal richness (Ding et al. 2025). Wang and Cai (2023) reported that 15,626 fungal taxa have been newly described from China, and that species recorded from China for the first time represent 6.84% of the currently documented global fungal diversity, placing China among the leading contributors worldwide. Newly described taxa are disproportionately reported from southwestern China (particularly Guizhou, Sichuan, Tibet and Yunnan) where complex topography and strong environmental gradients promote diversification and endemism (Yu et al. 2022; Zhang et al. 2023b; Hongsanan et al. 2023; Sun et al. 2024; Chen et al. 2025; Phurbu et al. 2025; Shen et al. 2025; Dissanayake et al. 2024a; Wanasinghe and Maharachchikumbura 2023; Wanasinghe et al. 2025). In addition, low-latitude tropical and subtropical regions, including Taiwan and Guangdong, also contribute substantially to national fungal diversity and continue to yield numerous novel and newly recorded taxa (Cheng et al. 2025; de Silva et al. 2025). In the present study, we focused on saprobic Sordariomycetes from woody litter in Yunnan, and based on morphological characteristics and multi-gene phylogenetic analyses, we introduce three new species and seven new records.

This study represents the first report of *Jattaea algeriensis* from China, where it was collected on dead woody twigs of *Myrsine seguinii* (Myrsinaceae). This species has previously been recorded in Algeria on decayed canes of *Rubus fruticosus*, South Africa on wood of *Prunus salicina* (Saccardo and Sydow 1902; Damm et al. 2008; Réblová 2011) and in Iran as a plant pathogen associated with *Mespilus germanica* and *Parrotia persica* (Kazemzadeh-Chakusary et al. 2020). The occurrence of *J. algeriensis* across geographically distant regions, contain North Africa, Southern Africa, the Middle East, and now East Asia, indicates that its distribution is likely broader than currently recorded and may be approaching a global scale. Given its confirmed pathogenicity on certain woody hosts in Iran, further understanding of the host range, environmental preferences, and transmission potential of *Jattaea algeriensis* is important for the prevention and control of the pathogen.

Phaeoacremonium camporesii (KUNCC 21-0608) and the ex-type strain of *P. camporesii* (MFLUCC 21-0224) exhibit a high degree of morphological similarity, particularly in the characteristics of the ascomata, asci, and ascospores. However, notable differences were observed in their stromatic development. The ex-type strain, *P. camporesii* (MFLUCC 21-0224), is capable of damaging the bark and forming conspicuous stromata on its surface, with numerous ascomata embedded within a single stroma. In contrast, our isolate (KUNCC 21-0608) does

not produce stromata on the bark surface, and its ascomata occur independently. Molecular comparisons further support the close relationship between the two isolates, yet also reveal subtle genetic variation (Phukhamsakda et al. 2022; this study). Comparative sequence analysis of the ITS and TUB regions showed that the ITS region is identical between the two strains, indicating strong genetic affinity. However, the TUB region exhibited a 5.4% nucleotide difference. As β-tubulin is a protein-coding gene that often shows higher levels of variation than ribosomal markers, this divergence may reflect intraspecific variability rather than species-level separation. The morphological similarity, the absence of ITS divergence, and the observed differences in TUB suggest that KUNCC 21-0608 should be regarded as a conspecific isolate of *P. camporesii*. The observed variation in stromatic development may be attributable to differences in environmental conditions, host interaction, or intraspecific phenotypic plasticity. This finding also highlights the importance of integrating morphological, ecological, and multilocus phylogenetic data for accurate fungal identification and classification.

The family Planisphaeriaceae currently comprises a single genus, *Planisphaeria*, which includes two species, *P. reniformispora* and *P. karsti* (Hyde et al. 2024b). In the present study, we report *P. karsti* and *P. reniformispora* from *Trigonobalanus doichangensis* (Fagaceae) for the first time, thereby expanding their known host range. Morphological and phylogenetic analyses confirm that our isolate of *P. karsti* (KUNCC 21-0543) is conspecific with the previously described strain GZAAS 20-4008. Both share the key morphological features of the species, including ascomata structure, asci morphology, and ascospore characteristics, and they cluster together in multi-gene phylogenetic analyses. Nonetheless, the two strains differ in ascospore shape, and the size ranges of both asci and ascospores (Zhang et al. 2023b; this study). Notably, KUNCC 21-0543 possesses reniform to allantoid ascospores, whereas GZAAS 20-4008 produces irregular ellipsoid ascospores with asymmetrical ends. A similar pattern of morphological divergence is evident between *P. reniformispora* isolates. Our isolate (KUNCC 21-0543) resembles with the type and they are phylogenetically closely affiliated. However, key differences were detected as GZAAS 20-4004 has reniform ascospores surrounded by a distinct mucilaginous sheath, while our isolate bears irregular ovoid, verrucose ascospores without a sheath and with abundant paraphyses (Zhang et al. 2023b; this study). These observations highlight that while molecular phylogeny provides robust species delimitation within *Planisphaeria*, intraspecific morphological variability can be substantial. Such variability may be influenced by ecological, host-related, or environmental factors, and further sampling across different geographic regions and hosts is needed to assess the stability and taxonomic significance of these micromorphological differences.

Barrmaelia was established by Rappaz (1995) to accommodate *B. rhamnicola* as the type species. Currently, nine epithets are recorded in Index Fungorum (2026), with a global distribution across Africa, Asia, Europe, and North America (Voglmayr et al. 2018; Dissanayake et al. 2024b). Except for *Barrmaelia serenoae*, which occurs on leaves, all other known species inhabit dead branches and stalk (Voglmayr et al. 2018; Crous et al. 2020; Dissanayake et al. 2024b). The genus is known only from its sexual morph, however, Crous et al. (2020) reported an asexual morph for *B. serenoae* (as a new species). In their study, the fungus from *Serenoa repens* was tentatively assigned to *Barrmaelia*. In our phylogenetic analyses, *B. serenoae* occupies a basal position, distinct from the

main *Barrmaelia* clade. This separation suggests that its phylogenetic placement within the genus remains uncertain and warrants further investigation. Moreover, the asexual morph of *Barrmaelia* is still poorly understood, further studies with additional collections are needed to understand the asexual morph.

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

Funding

This research was funded by the National Science Foundation of China (Grant No.: W2412011 and 32371785), and the Youth Innovation Promotion Association of CAS, China (Grant No.: 2022396). We would also like to thank the support from Central Government Guides Local Science and Technology Development Fund Projects (ZYYDDF2024-01), Agricultural Industry Integration Development Projects (GZFCG2026-31239), IAEA Coordinated Research Project (D15021) and the Yunnan Revitalization Talent Support Program "Young Talent" Project (XDYC-QNRC-2022-0346). We gratefully acknowledge the support of the Ongoing Research Funding Program (ORF-2026-487), King Saud University, Riyadh, Saudi Arabia. We also gratefully acknowledge support provided by Guizhou Provincial Administration of Traditional Chinese Medicine Research Project on Traditional Chinese Medicine and Ethnic Medicine (No.: QZYY-2025-220).

Author contributions

Data curation: ZYZ. Formal analysis: GCR, XS. Funding acquisition: TKF, DW, GCR, HG. Resources: HG. Software: KXD. Visualization: GCR. Writing – original draft: GCR. Writing – review and editing: DW.

Author ORCIDs

Guang-Cong Ren https://orcid.org/0000-0001-9923-2626
Dhanushka Wanasinghe https://orcid.org/0000-0003-1759-3933
Heng Gui https://orcid.org/0000-0002-0946-1589
Turki Kh. Faraj https://orcid.org/0000-0002-6012-8474

Data availability

All of the data that support the findings of this study are available in the main text.

References

Bao DF, Hyde KD, Maharachchikumbura SSN, Perera RH, Thiyagaraja V, Hongsanan S, Wanasinghe DN, Shen HW, Tian X, Yang LQ, Nalumpang S, Luo ZL (2023) Taxonomy, phylogeny and evolution of freshwater Hypocreomycetidae (Sordariomycetes). Fungal Diversity 121: 1–94. https://doi.org/10.1007/s13225-023-00521-8

Barr ME, Rogers JD, Ju YM (1993) Revisionary studies in the Calosphaeriaceae. Mycotaxon 48: 529–535. https://doi.org/10.5962/p.416449

Bebber S, Darrah P, Fricker M, Tlalka M, Boddy L (2006) The role of wood decay fungi in the carbon and nitrogen dynamics of the forest floor. In: Gadd G (Ed.) Fungi in Biogeochemical Cycles. Cambridge University Press, 151–181.

Berkeley MJ (1845) Decades of fungi. Decades III–VII. Australian fungi. London Journal of Botany 4: 42–73.

Bhilabutra W, Lumyong S, Jeewon R, McKenzie EHC, Hyde KD (2006) *Neolinocarpon penniseti* sp. nov. on the grass *Pennisetum purpureum* (Poaceae). Cryptogamie. Mycologie 27(4): 1–6.

Boddy L (2001) Fungal community ecology and wood decomposition processes in angiosperms: From standing tree to complete decay of coarse woody debris. Ecological Bulletins: 49–67.

Bucher VVC, Pointing SB, Hyde KD, Reddy CA (2004) Production of wood decay enzymes, loss of mass, and lignin solubilization in wood by diverse tropical freshwater fungi. Microbial Ecology 48: 331–337. https://doi.org/10.1007/s00248-003-0132-x

Calabon MS, Jones EBG, Boonmee S, Doilom M, Lumyong S, Hyde KD (2021) Five novel freshwater Ascomycetes indicate high undiscovered diversity in lotic habitats in Thailand. Journal of Fungi (Basel, Switzerland) 7(2): 117. https://doi.org/10.3390/jof7020117

Calabon MS, Bagacay JFE, Nim JA, Sadaba RB, Ferriols VMEN, Concha MJ, Velo J, Jones EG (2024) *Phaeoacremonium philippinense* (Togniniales, Sordariomycetes), a novel freshwater fungus from the Philippines. Phytotaxa 644(3): 177–189. https://doi.org/10.11646/PHYTOTAXA.644.3.1

Chaiwan N, Gomdola D, Wang S, Monkai J, Tibpromma S, Doilom M, Wanasinghe DN, Mortimer PE, Lumyong S, Hyde KD (2021) https://gmsmicrofungi.org: an online database providing updatedinformation of microfungi in the Greater Mekong Subregion. Mycosphere: Journal of Fungal Biology 12(1): 1513–1526. https://doi.org/10.5943/mycosphere/12/1/19

Chen ML, Zhang JY, Xiao YP, Lu YZ (2024) *Biscogniauxia dicranopteridis* sp. nov. and *B. petrensis* isolated from *Dicranopteris dichotoma* in China. Phytotaxa 641(4): 255–266. https://doi.org/10.11646/phytotaxa.641.4.2

Chen WH, Shu HL, Li D, Liang JD, Sun CL, Zhao JH, Wijayawardene NN, Han YF, Tian WY (2025) Shedding light on the darkness: Cryptic diversity of cordyceps-like fungi in karst regions of Guizhou Province, China. Mycosphere: Journal of Fungal Biology 16(1): 2887–2974. https://doi.org/10.5943/mycosphere/16/1/20

Chen YP, Su PW, Hyde KD, Maharachchikumbura SSN (2023) Phylogenomics and diversification of Sordariomycetes. Mycosphere 14(1): 414–451. https://doi.org/10.5943/mycosphere/14/1/5

Cheng KW, Ji Y, Srimongkol P, Stadler M, Karnchanatat A, Ariyawansa HA (2025) Fungal frontiers in toxic terrain: Revealing culturable fungal communities in Serpentine paddy fields of Taiwan. IMA Fungus 16: e155308. https://doi.org/10.3897/imafungus.16.155308

Chethana KWT, Rathnayaka AR, Samarakoon BC, Wu N, Wijesinghe SN, Yasanthika WAE, Sysouphanthong P, Thiyagaraja V, Armand A, Lestari AS, Madagammana AD, Ediriweera AN, Prematunga C, Li CJY, Tennakoon DS, Gomdola D, Marasinghe DS, Bundhun D, Pem D, Ren GC, Zhao H, Su H, Win H, Li H, Lu L, Calabon MS, Samarakoon MC, Chaiwan N, Huanraluek N, Samaradiwakara NP, Kularathnage ND, Abeywickrama PD, Perera RH, Tang SM, Du TY, Punyaboon W, Ma X, Yang Y, Tun ZL, Bhunjun CS,

Manawasinghe IS, Senanayake IC, Liu JK, Tibpromma S, Wadduwage KS, Wijayalath WHDN, Raspé O, Bulgakov TS, Camporesi E, Promputtha I, Hyde KD (2023) AJOM new records and collections of fungi: 151–200. Asian Journal of Mycology 6(2): 89–243. https://doi.org/10.5943/ajom/6/2/7

Crous PW, Gams W, Wingfield MJ, Van Wyk PS (1996) *Phaeoacremonium* gen. nov. associated with with and decline diseases of woody hosts and human infections. Mycologia 88: 786–796. https://doi.org/10.1080/00275514.1996.12026716

Crous PW, Wingffeld MJ, Schumacher RK, Akulov A, Bulgakov TS, Carnegie AJ, Jurjević Ž, Decock C, Denman S, Lombard L, Lawrence DP, Stack AJ, Gordon TR, Bostock RM, Burgess T, Summerell BA, Taylor PWJ, Edwards J, Hou LW, Cai L, Rossman AY, Wöhner T, Allen WC, Castlebury LA, Visagie CM, Groenewald JZ (2020) New and Interesttng Fungi. 3. Fungal Systemattcs and Evolutton 6: 157–231. https://doi.org/10.3114/fuse.2020.06.09

Crous PW, Wingfield MJ, Jurjević Ž, Balashov S, Osieck ER, Marin-Felix Y, Luangsa-ard JJ, Mejía LC, Cappelli A, Parra LA, Lucchini G, Chen J, Moreno G, Faraoni M, Zhao RL, Weholt Ø, Borovička J, Jansen GM, Shivas RG, Tan YP, Akulov A, Alfenas AC, Alfenas RF, Altés A, Avchar R, Barreto RW, Catchside DEA, Chi TY, Esteve-Raventós F, Fryar SC, Hanh LTM, Larsbrink J, Oberlies NH, Olsson L, Pancorbo F, Raja HA, Thanh VN, Thuy NT, Ajithkumar K, Akram W, Alvarado P, Angeletti B, Arumugam E, Khalilabad AA, Bandini D, Baroni T, Barreto GG, Bortmann G, Bose T, Castañeda-Ruiz RF, Couceiro A, Cykowska-Marzcenka B, Cabral YC, Darmostuk V, da Silva SBG, Dearnaley JDW, de Azevedo Santiago ALCM, Declercq B, de Freitas LWS, de la Peña-Lastra S, Delgado G, de Lima CLF, Dhotre D, Dirks AC, Eisvand P, Erhard A, Ferro LO, García D, García-Martín A, Garrido-Benavent I, Gené J, Ghodad-Nejhad M, Gore G, Gusmão LFP, Hammerbacher A, Hernández-Perez AT, Hernández-Restrepo M, Hofmann TA, Hubka V, Jiya N, Kaliyaperumal M, Keerthanan KS, Kethabi M, Kezo K, Knoppsersen R, Kolarczyková D, Kumar TKA, Læssøe T, Langer E, Larsson E, Lodge DJ, Lynch MJ, Maciá-Vicente JG, Mahadevakumar S, Mateos A, Mehrabi-Koushki M, Miglio BV, Noor A, Oliveira JA, Pallez OL, Piątek M, Pinto A, Ramírez GH, Raphael B, Rawat G, Renuka R, Reschke K, Ruiz Mateo A, Saar I, Saba M, Safi A, Sánchez RM, Sandoval-Denis M, Savitha AS, Sharma A, Shelke D, Sonawane H, Souza MGP, Stryjak-Bogacka M, Thines M, Thomas A, Torres-Garcia D, Traba JM, Vauras J, Vermaas M, Villarreal M, Vu D, Whiteside EJ, Zafari D, Starink-Willemse M, Groenewald JZ (2024) Fungal Planet description sheets: 1697–1780. Fungal Systematics and Evolution 14: 325–577. https://doi.org/10.3114/fuse.2024.14.19

Dai YC, Cui BK, Si J, He SH, Hyde KD, Yuan HS, Liu XY, Zhou LW (2015) Dynamics of the worldwide number of fungi with emphasis on fungal diversity in China. Mycological Progress 14(8): 62. https://doi.org/10.1007/s11557-015-1084-5

Damm U, Crous PW, Fourie PH (2008) A fssitunicate ascus mechanism in the Calosphaeriaceae, with novel species of *Jattaea* and *Calosphaeria* on *Prunus* wood. Persoonia 20: 39–52. https://doi.org/10.3767/003158508x313940

de Silva NI, Tennakoon DS, Xie N, Hongsanan S (2025) Taxonomic novelties in Dictyosporiaceae and Pleurotremataceae (Dothideomycetes, Ascomycota): Two new species and three new host reports in the coastal region of Guangdong Province, China. MycoKeys 125: 115–146. https://doi.org/10.3897/mycokeys.125.171612

Delavaux CS, LaManna JA, Myers JA, Phillips RP, Aguilar S, Allen D, Alonso A, Anderson-Teixeira KJ, Baker ME, Baltzer JL, Bissiengou P, Bonfim M, Bourg NA, Brockelman WY, Burslem DFRP, Chang LW, Chen Y, Chiang JM, Chu C, Clay K, Cordell S, Cortese M, den Ouden J, Dick C, Ediriweera S, Ellis EC, Feistner A, Freestone AL, Giambelluca T,

Giardina CP, Gilbert GS, He F, Holík J, Howe RW, Huaraca Huasca W, Hubbell SP, Inman F, Jansen PA, Johnson DJ, Kral K, Larson AJ, Litton CM, Lutz JA, Malhi Y, McGuire K, McMahon SM, McShea WJ, Memiaghe H, Nathalang A, Norden N, Novotny V, O'Brien MJ, Orwig DA, Ostertag R, Parker GG, Pérez R, Reynolds G, Russo SE, Sack L, Šamonil P, Sun IF, Swanson ME, Thompson J, Uriarte M, Vandermeer J, Wang X, Ware I, Weiblen GD, Wolf A, Wu SH, Zimmerman JK, Lauber T, Maynard DS, Crowther TW, Averill C (2023) Mycorrhizal feedbacks influence global forest structure and diversity. Communications Biology 6(1): 1066. https://doi.org/10.1038/s42003-023-05410-z

Ding ZY, Ji XY, Li F, Liu WX, Wang S, Zhao H, Liu XY (2025) Unveiling species diversity within early-diverging Fungi from China IX: Four new species of *Mucor* (Mucoromycota). Journal of Fungi (Basel, Switzerland) 11(9): 682. https://doi.org/10.3390/jof11090682

Dissanayake LS, Phookamsak R, Xu J, Wanasinghe DN (2024a) *Oxydothis ailaoshanensis* sp. nov. (Oxydothidaceae, Xylariales) from dead bamboo culms in Yunnan Province, China. Studies in Fungi 9: e016. https://doi.org/10.48130/sif-0024-0016

Dissanayake LS, Samarakoon MC, Maharachchikumbura SSN, Hyde KD, Tang X, Li QR, Mortimer PE, Faraj TK, Xu JC, Kang JC, Wanasinghe DN (2024b) Exploring the taxonomy and phylogeny of Sordariomycetes taxa emphasizing Xylariomycetidae in Southwestern China. Mycosphere: Journal of Fungal Biology 15(1): 1675–1793. https://doi.org/10.5943/mycosphere/15/1/15

Ekanayaka AH, Karunarathna SC, Tibpromma S, Dutta AK, Tennakoon DS, Karunarathna A, Chukeatirote E, Dai DQ, Stephenson SL, Maharachchikumbura SSN, Liu C, Phillips AJL (2025) Species evolution: Cryptic species and phenotypic noise with a particular focus on fungal systematics. Frontiers in Cellular and Infection Microbiology 15: 1497085. https://doi.org/10.3389/fcimb.2025.1497085

Esfandiari E, Petrak F (1950) Pilze aus Iran. Sydowia 4: 31–38.

Feng B, Yang Z (2018) Studies on diversity of higher fungi in Yunnan southwestern China: A review. Plant Diversity 40: 165–690. https://doi.org/10.1016/j.pld.2018.07.001

Fuckel L (1870) Symbolae mycologicae. Beiträge zur Kenntniss der Rheinischen Pilze. Jahrbücher Des Nassauischen Vereins Für Naturkunde 23–24: 1–459. https://doi.org/10.5962/bhl.title.47117

Fukasawa Y (2021) Ecological impacts of fungal wood decay types: A review of current knowledge and future research directions. Ecological Research 36(6): 910–931. https://doi.org/10.1111/1440-1703.12260

Fukasawa Y, Osono T, Takeda H (2011) Wood decomposing abilities of diverse lignicolous fungi on nondecayed and decayed beech wood. Mycologia 103: 474–482. https://doi.org/10.3852/10-246

Gautam AK, Verma RK, Avasthi S, Sushma, Bohra Y, Devadatha B, Niranjan M, Suwannarach N (2022) Current Insight into Traditional and Modern Methods in Fungal Diversity Estimates. Journal of Fungi (Basel, Switzerland) 8(3): 226. https://doi.org/10.3390/jof8030226

Habib K, Li WH, Ren YL, Liu LL, Lu CT, Zhang QF, Yao ZQ, Luo XY, Zhou X, Zeng WY, Kang YQ, Shen XC, Wijayawardene NN, Elgorban AM, Al-Rejaie S, Li QR (2025) Exploration of ascomycetous fungi revealing novel taxa in Southwestern China. Mycosphere: Journal of Fungal Biology 16(1): 1412–1529. https://doi.org/10.5943/mycosphere/16/1/9

Hall TA (1999) BioEdit: A user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41: 95–98.

Hongsanan S, Phookamsak R, Bhat DJ, Wanasinghe DN, Promputtha I, Suwannarach N, Sandamali D, Lumyong S, Xu J, Xie N (2023) Exploring ascomycete diversity in

Yunnan, China I: Resolving ambiguous taxa in Phaeothecoidiellaceae and investigating conservation implications of fungi. Frontiers in Cellular and Infection Microbiology 13: 1252387. https://doi.org/10.3389/fcimb.2023.1252387

Huang SK, Hyde KD, Mapook A, Maharachchikumbura SSN, Bhat JD, McKenzie EHC, Jeewon R, Wen TC (2021) Taxonomic studies of some often over-looked Diaporthomycetidae and Sordariomycetidae. Fungal Diversity 111: 443–572. https://doi.org/10.1007/s13225-021-00488-4

Hyde KD (1992) Fungi from decaying intertidal fronds of *Nypa fruticans*, including three new genera and four new species. Botanical Journal of the Linnean Society 110: 95–110. https://doi.org/10.1111/j.1095-8339.1992.tb00284.x

Hyde KD, Alias SA (1999) *Linocarpon angustatum* sp. nov., and *Neolinocarpon nypicola* sp. nov. from petioles of *Nypa fruticans*, and a list of fungi from aerial parts of this host. Mycoscience 40: 145–149. https://doi.org/10.1007/BF02464293

Hyde KD, Taylor JE, Fröhlich J (1998) Fungi from palms. XXXIV. The genus *Neolinocarpon* with five new species and one new combination. Fungal Diversity 1: 115–131.

Hyde KD, Xu JC, Lumyong S, Rapior S, Jeewon R, Niego AGT, Abeywickrama PD, Aluthmuhandiram JVS, Brahamanage RS, Brooks S, Chaiyasen A, Chethana KWT, Chomnunti P, Chepkirui C, Chuankid B, de Silva NI, Doilom M, Faulds C, Gentekaki E, Gopalan V, Kakumyan P, Harishchandra D, Hemachandran H, Hongsanan S, Karunarathna A, Karunarathna SC, Khan S, Kumla J, Jayawardena RS, Liu JK, Liu N, Luangharm T, Macabeo APG, Marasinghe DS, Meeks D, Mortimer PE, Mueller P, Nadir S, Nataraja KN, Nontachaiyapoom S, O'Brien M, Penkhrue W, Phukhamsakda C, Ramanan US, Rathnayaka AR, Sadaba RB, Sandargo B, Samarakoon BC, Tennakoon DS, Siva R, Sriprom W, Suryanarayanan TS, Sujarit K, Suwannarach N, Suwunwong T, Thongbai B, Thongklang N, Wei D, Wijesinghe SN, Winiski J, Yan J, Yasanthika E, Stadler M (2019) The amazing potential of fungi, 50 ways we can exploit fungi industrially. Fungal Diversity 97: 1–136. https://doi.org/10.1007/s13225-019-00430-9

Hyde KD, Dong Y, Phookamsak R, Jeewon R, Bhat DJ, Jones EBG, Liu NG, Abeywickrama PD, Mapook A, Wei DP, Perera RH, Manawasinghe IS, Pem D, Bundhun D, Karunarathna A, Ekanayaka AH, Bao DF, Li JF, Samarakoon MC, Chaiwan N, Lin CG, Phutthacharoen K, Zhang SN, Senanayake IC, Goonasekara ID, Thambugala KM, Phukhamsakda C, Tennakoon DS, Jiang HB, Yang J, Zeng M, Huanraluek N, Liu JK, Wijesinghe SN, Tian Q, Tibpromma S, Brahmanage RS, Boonmee S, Huang SK, Thiyagaraja V, Lu YZ, Jayawardena RS, Dong W, Yang EF, Singh SK, Singh SM, Rana S, Lad SS, Anand G, Devadatha B, Niranjan M, Sarma VV, Liimatainen K, Aguirre-Hudson B, Niskanen T, Overall A, Alvarenga RLM, Gibertoni TB, Pfiegler WP, Horváth E, Imre A, Alves AL, da Silva Santos AC, Tiago PV, Bulgakov TS, Wanasinghe DN, Bahkali AH, Doilom M, Elgorban AM, Maharachchikumbura SSN, Rajeshkumar KC, Haelewaters D, Mortimer PE, Zhao Q, Lumyong S, Xu JC, Sheng J (2020a) Fungal Diversity notes 1151–1276: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 100: 5–277. https://doi.org/10.1007/s13225-020-00439-5

Hyde KD, Norphanphoun C, Maharachchikumbura SSN, Bhat DJ, Jones EBG, Bundhun D, Chen YJ, Bao DF, Boonmee S, Calabon MS, Chaiwan N, Chethana KWT, Dai DQ, Dayarathne MC, Devadatha B, Dissanayake AJ, Dissanayake LS, Doilom M, Dong W, Fan XL, Goonasekara ID, Hongsanan S, Huang SK, Jayawardena RS, Jeewon R, Karunarathna A, Konta S, Kumar V, Lin CG, Liu JK, Liu NG, Luangsa-ard J, Lumyong S, Luo ZL, Marasinghe DS, McKenzie EHC, Niego AGT, Niranjan M, Perera RH, Phukhamsakda C, Rathnayaka AR, Samarakoon MC, Samarakoon SMBC, Sarma VV, Senanayake IC, Shang QJ, Stadler M, Tibpromma S, Wanasinghe DN, Wei DP, Wijayawardene

NN, Xiao YP, Yang J, Zeng XY, Zhang SN, Xiang MM (2020b) Refined families of Sordariomycetes. Mycosphere: Journal of Fungal Biology 11(1): 305–1059. https://doi.org/10.5943/mycosphere/11/1/7

Hyde KD, Baldrian P, Chen Y, Chethana KWT, De Hoog S, Doilom M, Gomes de Farias AR, Gonçalves MFM, Gonkhom D, Gui H, Hilário S, Hu Y, Jayawardena RS, Khyaju S, Kirk PM, Kohout P, Luangharn T, Maharachchikumbura SSN, Manawasinghe IS, Mortimer PE, Niego AGT, Phonemany M, Sandargo B, Senanayake IC, Stadler M, Surup F, Thongklang N, Wanasinghe DN, Bahkali AH, Walker A (2024a) Current trends, limitations and future research in the fungi? Fungal Diversity 125(1): 1–71. https://doi.org/10.1007/s13225-023-00532-5

Hyde KD, Noorabadi MT, Thiyagaraja V, He MQ, Johnston PR, Wijesinghe SN, Armand A, Biketova AY, Chethana KWT, Erdoğdu M, Ge ZW, Groenewald JZ, Hongsanan S, Kušan I, Leontyev DV, Li DW, Lin CG, Liu NG, Maharachchikumbura SSN, Matočec N, May TW, McKenzie EHC, Mešić A, Perera RH, Phukhamsakda C, Piątek M, Samarakoon MC, Selcuk F, Senanayake IC, Tanney JB, Tian Q, Vizzini A, Wanasinghe DN, Wannasawang N, Wijayawardene NN, Zhao RL, Abdel-Wahab MA, Abdollahzadeh J, Abeywickrama PD, Abhinav, Absalan S, Acharya K, Afshari N, Afshan NS, Afzalinia S, Ahmadpour SA, Akulov O, Alizadeh A, Alizadeh M, Al-Sadi AM, Alves A, Alves VCS, Alves-Silva G, Antonín V, Aouali S, Aptroot A, Apurillo CCS, Arias RM, Asgari B, Asghari R, Assis DMA, Assyov B, Atienza V, Aumentado HDR, Avasthi S, Azevedo E, Bakhshi M, Bao DF, Baral HO, Barata M, Barbosa KD, Barbosa RN, Barbosa FR, Baroncelli R, Barreto GG, Baschien C, Bennett RM, Bera I, Bezerra JDP, Bhunjun CS, Bianchinotti MV, Błaszkowski J, Boekhout T, Bonito GM, Boonmee S, Boonyuen N, Bortnikov FM, Bregant C, Bundhun D, Burgaud G, Buyck B, Caeiro MF, Cabarroi-Hernández M, Cai MF, Cai L, Calabon MS, Calaça FJS, Callalli M, Câmara MPS, Cano-Lira J, Cao B, Carlavilla JR, Carvalho A, Carvalho TG, Castañeda-Ruiz RF, Catania MDV, Cazabonne J, Cedeño-Sanchez M, Chaharmiri-Dokhaharani S, Chaiwan N, Chakraborty N, Cheewankoon R, Chen C, Chen J, Chen Q, Chen YP, Chinaglia S, Coelho-Nascimento CC, Coleine C, Costa-Rezende DH, Cortés-Pérez A, Crouch JA, Crous PW, Cruz RHSF, Czachura P, Damm U, Darmostuk V, Daroodi Z, Das K, Das K, Davoodian N, Davydov EA, da Silva GA, da Silva IR, da Silva RMF, da Silva Santos AC, Dai DQ, Dai YC, de Groot Michiel D, De Kesel A, De Lange R, de Medeiros EV, de Souza CFA, de Souza FA, dela Cruz TEE, Decock C, Delgado G, Denchev CM, Denchev TT, Deng YL, Dentinger BTM, Devadatha B, Dianese JC, Dima B, Doilom M, Dissanayake AJ, Dissanayake DMLS, Dissanayake LS, Diniz AG, Dolatabadi S, Dong JH, Dong W, Dong ZY, Drechsler-Santos ER, Druzhinina IS, Du TY, Dubey MK, Dutta AK, Elliott TF, Elshahed MS, Egidi E, Eisvand P, Fan L, Fan X, Fan XL, Fedosova AG, Ferro LO, Fiuza PO, Flakus AW, Fonseca EO, Fryar SC, Gabaldón T, Gajanayake AJ, Gannibal PB, Gao F, García-Sánchez D, García-Sandoval R, Garrido-Benavent I, Garzoli L, Gasca-Pineda J, Gautam AK, Gené J, Ghobad-Nejhad M, Ghosh A, Giachini AJ, Gibertoni TB, Gentekaki E, Gmoshinskiy VI, Góes-Neto A, Gomdola D, Gorjón SP, Goto BT, Granados-Montero MM, Griffith GW, Groenewald M, Grossart H-P, Gu ZR, Gueidan C, Gunarathne A, Gunaseelan S, Guo SL, Gusmão LFP, Gutierrez AC, Guzmán-Dávalos L, Haelewaters D, Haituk H, Halling RE, He SC, Heredia G, Hernández-Restrepo M, Hosoya T, Hoog SD, Horak E, Hou CL, Houbraken J, Htet ZH, Huang SK, Huang WJ, Hurdeal VG, Hustad VP, Inácio CA, Janik P, Jayalal RGU, Jayasiri SC, Jayawardena RS, Jeewon R, Jerônimo GH, Jin J, Jones EBG, Joshi Y, Jurjević Ž, Justo A, Kakishima M, Kaliyaperumal M, Kang GP, Kang JC, Karimi O, Karunarathna SC, Karpov SA, Kezo K, Khalid AN, Khan MK, Khuna S, Khyaju S, Kirchmair M, Klawonn I, Kraisitudomsook N, Kukwa M, Kularathnage ND, Kumar S, Lachance MA, Lado C, Latha KPD, Lee HB, Leonardi M, Lestari AS, Li C, Li H,

Li J, Li Q, Li Y, Li YC, Li YX, Liao CF, Lima JLR, Lima JMS, Lima NB, Lin L, Linaldeddu BT, Linn MM, Liu F, Liu JK, Liu JW, Liu S, Liu SL, Liu XF, Liu XY, Longcore JE, Luangharn T, Luangsa-ard JJ, Lu L, Lu YZ, Lumbsch HT, Luo L, Luo M, Luo ZL, Ma J, Madagammana AD, Madhushan A, Madrid H, Magurno F, Magyar D, Mahadevakumar S, Malosso E, Malysh JM, Mamarabadi M, Manawasinghe IS, Manfrino RG, Manimohan P, Mao N, Mapook A, Marchese P, Marasinghe DS, Mardones M, Marin-Felix Y, Masigol H, Mehrabi M, Mehrabi-Koushki M, Meiras-Ottoni A de, Melo RFR, Mendes-Alvarenga RL, Mendieta S, Meng QF, Menkis A, Menolli Jr N, Mikšík M, Miller SL, Moncada B, Moncalvo JM, Monteiro JS, Monteiro M, Mora-Montes HM, Moroz EL, Moura JC, Muhammad U, Mukhopadhyay S, Nagy GL, Najam ul Sehar A, Najafiniya M, Nanayakkara CM, Naseer A, Nascimento ECR, Nascimento SS, Neuhauser S, Neves MA, Niazi AR, Nie Y, Nilsson RH, Nogueira PTS, Novozhilov YK, Noordeloos M, Norphanphoun C, Nuñez Otaño N, O'Donnell RP, Oehl F, Oliveira JA, Oliveira Junior I, Oliveira NVL, Oliveira PHF, Orihara T, Oset M, Pang KL, Papp V, Pathirana LS, Peintner U, Pem D, Pereira OL, Pérez-Moreno J, Pérez-Ortega S, Péter G, Pires-Zottarelli CLA, Phonemany M, Phongeun S, Pošta A, Prazeres JFSA, Quan Y, Quandt CA, Queiroz MB, Radek R, Rahnama K, Raj KNA, Rajeshkumar KC, Rajwar S, Ralaiveloarisoa AB, Rämä T, Ramírez-Cruz V, Rambold G, Rathnayaka AR, Raza M, Ren GC, Rinaldi AC, Rivas-Ferreiro M, Robledo GL, Ronikier A, Rossi W, Rusevska K, Ryberg M, Safi A, Salimi F, Salvador-Montoya CA, Samant B, Samaradiwakara NP, Sánchez-Castro I, Sandoval-Denis M, Santiago ALCMA, Santos ACDS, Santos LA dos, Sarma VV, Sarwar S, Savchenko A, Savchenko K, Saxena RK, Schoutteten N, Selbmann L, Ševčíková H, Sharma A, Shen HW, Shen YM, Shu YX, Silva HF, Silva-Filho AGS, Silva VSH, Simmons DR, Singh R, Sir EB, Sohrabi M, Souza FA, Souza-Motta CM, Sri-indrasutdhi V, Sruthi OP, Stadler M, Stemler J, Stephenson SL, Stoyneva-Gaertner MP, Strassert JFH, Stryjak-Bogacka M, Su H, Sun YR, Svantesson S, Sysouphanthong P, Takamatsu S, Tan TH, Tanaka K, Tang C, Tang X, Taylor JE, Taylor PWJ, Tennakoon DS, Thakshila SAD, Thambugala KM, Thamodini GK, Thilanga D, Thines M, Tiago PV, Tian XG, Tian WH, Tibpromma S, Tkalčec Z, Tokarev YS, Tomšovský M, Torruella G, Tsurykau A, Udayanga D, Ulukapı M, Untereiner WA, Usman M, Uzunov BA, Vadthanarat S, Valenzuela R, Van den Wyngaert S, Van Vooren N, Velez P, Verma RK, Vieira LC, Vieira WAS, Vinzelj JM, Tang AMC, Walker A, Walker AK, Wang QM, Wang Y, Wang XY, Wang ZY, Wannathes N, Wartchow F, Weerakoon G, Wei DP, Wei X, White JF, Wijesundara DSA, Wisitrassameewong K, Worobiec G, Wu HX, Wu N, Xiong YR, Xu B, Xu JP, Xu R, Xu RF, Xu RJ, Yadav S, Yakovchenko LS, Yang HD, Yang X, Yang YH, Yang Y, Yang YY, Yoshioka R, Youssef Noha H, Yu FM, Yu ZF, Yuan LL, Yuan Q, Zabin DA, Zamora JC, Zapata CV, Zare R, Zeng M, Zeng XY, Zhang JF, Zhang JY, Zhang S, Zhang XC, Zhao CL, Zhao H, Zhao Q, Zhao H, Zhao HJ, Zhou HM, Zhu XY, Zmitrovich IV, Zucconi L, Zvyagina E (2024b) The 2024 Outline of Fungi and fungus-like taxa. Mycosphere: Journal of Fungal Biology 15(1): 5146–6239. https://doi.org/10.5943/mycosphere/15/1/25

Index Fungorum (2026) Index Fungorum. http://www.indexfungorum.org/Names/Names.asp [Accessed on 31st January 2026]

Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat J, Buyck B, Cai L, Dai YC, Abd-Elsalam KA, Ertz D, Hidayat I, Jeewon R, Jones EBG, Bahkali AH, Karunarathna SC, Liu JK, Luangsa-ard JJ, Lumbsch HT, Maharachchikumbura SSN, McKenzie EHC, Moncalvo JM, Ghobad-Nejhad M, Nilsson H, Pang KA, Pereira OL, Phillips AJL, Raspé O, Rollins AW, Romero AI, Etayo J, Selçuk F, Stephenson SL, Suetrong S, Taylor JE, Tsui CKM, Vizzini A, Abdel-Wahab MA, Wen TC, Boonmee S, Dai DQ, Daranagama DA, Dissanayake AJ, Ekanayaka AH, Fryar SC, Hongsanan S, Jayawardena RS, Li WJ, Perera RH, Phookamsak R, de Silva NI, Thambugala KM, Tian Q, Wijayawardene NN, Zhao RL,

Zhao Q, Kang JC, Promputtha I (2015) The Faces of Fungi database: Fungal names linked with morphology, phylogeny and human impacts. Fungal Diversity 74(1): 3–18. https://doi.org/10.1007/s13225-015-0351-8

Ju YM, Rogers JD (2001) New and interesting *Biscogniauxia* taxa, with a key to the world species. Mycological Research 105: 1123–1133. https://doi.org/10.1016/s0953-7562(08)61976-0

Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics 20(4): 1160–1166. https://doi.org/10.1093/bib/bbx108

Kazemzadeh-Chakusary M, Mohammadi H, Sohrabi M (2020) Occurrence and pathogenicity of *Jattaea algeriensis* (Calosphaeriales, Calosphaeriaceae) and *Biscogniauxia mediterranea* on forest trees in Guilan Province (Iran). Journal of Phytopathology 169(2): 129–138. https://doi.org/10.1111/jph.12967

Konta S, Hongsanan S, Eungwanichayapant PD, Liu JK, Jeewon R, Hyde KD, Maharachchikumbura SSN, Boonmee S (2017) *Leptosporella* (Leptosporellaceae fam. nov.) and *Linocarpon* and *Neolinocarpon* (Linocarpaceae fam. nov.) are accommodated in Chaetosphaeriales. Mycosphere: Journal of Fungal Biology 8(10): 1943–1974. https://doi.org/10.5943/mycosphere/8/10/16

Leonardi GR, Aiello D, Di Pietro C, Gugliuzzo A, Tropea Garzia G, Polizzi G, Voglmayr H (2024) *Thyridium lauri* sp. nov. (Thyridiaceae, Thyridiales): A new pathogenic fungal species of bay laurel from Italy. MycoKeys 110: 211–236. https://doi.org/10.3897/mycokeys.110.129228

Lim SK, Azmi MH, Kim MK, Kim SH, Lee SY, Jung HY (2025) A novel *Phaeoacremonium* species isolated from Galls on the Chinese Magnolia-Vine (Schisandra chinensis) in Korea. Mycobiology 53(2): 243–249. https://doi.org/10.1080/12298093.2024.2438463

Liu YJ, Whelen S, Hall BD (1999) Phylogenetic relationships among ascomycetes: Evidence from an RNA polymerse II subunit. Molecular Biology and Evolution 16(12): 1799–1808. https://doi.org/10.1093/oxfordjournals.molbev.a026092

Lonsdale D, Pautasso M, Holdenrieder O (2008) Wood-decaying fungi in the forest: Conservation needs and management options. European Journal of Forest Research 127: 1–22. https://doi.org/10.1007/s10342-007-0182-6

Luo ZL, Hyde KD, Liu JK, Maharachchikumbura SSN, Jeewon R, Bao DF, Bhat DJ, Lin CG, Li WL, Yang J, Liu NG, Lu YZ, Jayawardena RS, Li JF, Su HY (2019) Freshwater sordariomycetes. Fungal Diversity 99: 451–660. https://doi.org/10.1007/s13225-019-00438-1

Luo X, Lu C, Habib K, Ren Y, Jin Y, Li W, Lu P, Kang Y, Shen X, Al-Shwaiman HA, Elgorban AM, Wijayawardene NN, Chen Y, Li Q (2025) New species of *Vamsapriya* (Vamsapriyaceae, Xylariales) and *Neolinocarpon* (Linocarpaceae, Chaetosphaeriales) from Yunnan, China. MycoKeys 120: 173–192. https://doi.org/10.3897/mycokeys.120.156619

Lustenhouwer N, Maynard DS, Bradford MA, Lindner DL, Oberle B, Zanne AE, Crowther TW (2020) A trait-based understanding of wood decomposition by fungi. Proceedings of the National Academy of Sciences of the United States of America 117(21): 11551–11558. https://doi.org/10.1073/pnas.1909166117

Maharachchikumbura SSN, Hyde KD, Jones EBG, McKenzie EHC, Huang SK, Abdel-Wahab MA, Daranagama DA, Dayarathne M, D'souza MJ, Goonasekara ID, Hongsanan S, Jayawardena RS, Kirk PM, Konta S, Liu JK, Liu ZY, Norphanphoun C, Pang KL, Perera RH, Senanayake IC, Shang QJ, Shenoy BD, Xiao YP, Bahkali AH, Kang JC, Somrothipol S, Suetrong S, Wen TC, Xu JC (2015) Towards a natural classifcation and backbone tree for Sordariomycetes. Fungal Diversity 72: 199–301. https://doi.org/10.1007/s13225-015-0331-z

Maharachchikumbura SSN, Hyde KD, Jones EBG, McKenzie EHC, Bhat JD, Dayarathee MC, Huang SK, Norphanphoun C, Senanayake IC, Perera RH, Shang QJ, Xiao YP, D'souza MJ, Hongsanan S, Jayawardena RS, Daranagama DA, Konta S, Goonasekara ID, Zhuang WY, Jeewon R, Phillips AJL, Abdel-Wahab MA, Al-Sadi AM, Bahkali AH, Boonnee S, Boonyuen N, Cheewangkoon R, Dissanayake AJ, Kang J, Li QR, Liu JK, Liu XZ, Liu ZY, Luangsa-ard JJ, Pang KL, Phookamsak R, Promputtha I, Suetrong S, Stadler M, Wen TC, Wijayawardene NN (2016) Families of sordariomycetes. Fungal Diversity 79: 1–317. https://doi.org/10.1007/s13225-016-0369-6

Manawasinghe IS, Calabon MS, Jones EBG, Zhang YX, Liao CF, Xiong Y, Chaiwan N, Kularathnage ND, Liu NG, Tang SM, Sysouphanthong P, Du TY, Luo M, Pasouvang P, Pem D, Phonemany M, Ishaq M, Chen JW, Karunarathna SC, Mai ZL, Rathnayaka AR, Samarakoon MC, Tennakoon DS, Wijesinghe SN, Yang YH, Zhao HJ, Fiaz M, Doilom M, Dutta AK, Khalid AN, Liu JW, Thongklang N, Senanayake IC, Tibpromma S, You LQ, Camporesi E, Gafforov YS, Hyde KD (2022) Mycosphere notes 345–386. Mycosphere: Journal of Fungal Biology 13(1): 454–557. https://doi.org/10.5943/mycosphere/13/1/3

Marcot BG (2017) A review of the role of fungi in wood decay of forest ecosystems. US Department of Agriculture, Forest Service, Pacific Northwest Research Station. https://doi.org/10.2737/pnw-rn-575

Miller AN, Huhndorf SM (2005) Multi-gene phylogenies indicate ascomal wall morphology is a better predictor of phylogenetic relationships than ascospore morphology in the Sordariales (Ascomycota, Fungi). Molecular Phylogenetics and Evolution 35(1): 60–75. https://doi.org/10.1016/j.ympev.2005.01.007

Miller MA, Pfeiffer W, Schwartz T (2010) Creating the CIPRES Science Gateway for inference of large phylogenetic trees. Proceedings of the Gateway Computing Environments Workshop (GCE). New Orleans, LA, 1–8. https://doi.org/10.1109/GCE.2010.5676129

Monkai J, Promputtha I, Kodsueb R, Chukeatirote E, McKenzie EHC, Hyde KD (2013) Fungi on decaying leaves of *Magnolia liliifera* and *Cinnamomum iners* show litter fungi to be hyperdiverse. Mycosphere: Journal of Fungal Biology 4(2): 292–301. https://doi.org/10.5943/mycosphere/4/2/12

Mostert L, Crous PW, Groenewald JZ, Gams W, Summerbell RC (2003) *Togninia* (Calosphaeriales) is confrmed as teleomorph of *Phaeoacremonium* by means of morphology, sexual compatibility and DNA phylogeny. Mycologia 95: 646–659. https://doi.org/10.2307/3761941

Mostert L, Groenewald JZ, Summerbell RC, Gams W, Crous PW (2006) Taxonomy and pathology of *Togninia* (Diaporthales) and its *Phaeoacremonium* anamorphs. Studies in Mycology 54: 1–113. https://doi.org/10.3114/sim.54.1.1

Mostert L, Whipp M, Woodgyer A, Summerbell RC, Gramaje D, Spies CFJ (2024) *Phaeoacremonium tuscanicum* and *Phaeoacremonium indicum* sp. nov. associated with subcutaneous phaeohyphomycosis. Mycology 15(1): 129–135. https://doi.org/10.1080/21501203.2024.2312917

Munk A (1957) Danish Pyrenomycetes. A preliminary flora. Dansk Botanisk Arkiv 17(1): 1–491.

Nitschke T (1867) Pyrenomycetes Germanici. Die Kernpilze Deutschlands. 1: 1–160. Eduard Trewendt, Breslau. https://hdl.handle.net/2027/coo.31924000644199

Nylander JAA, Wilgenbusch JC, Warren DL, Swofford DL (2008) AWTY: A system for graphical exploration of MCMC convergence in Bayesian phylogenetics. Bioinformatics (Oxford, England) 24(4): 581–583. https://doi.org/10.1093/bioinformatics/btm388

O'Donnell K, Cigelnik E (1997) Two divergent intragenomic rDNA ITS2 types within amonophyletic lineage of the fungus Fusarium are nonorthologous. Molecular Phylogenetics and Evolution 7: 103–116. https://doi.org/10.1006/mpev.1996.0376

Phookamsak R, Hongsanan S, Bhat DJ, Wanasinghe DN, Promputtha I, Suwannarach N, Kumla J, Xie N, Dawoud TM, Mortimer PE, Xu JC, Lumyong S (2024) Exploring ascomycete diversity in Yunnan II: Introducing three novel species in the suborder Massarineae (Dothideomycetes, Pleosporales) from fern and grasses. MycoKeys 104: 9. https://doi.org/10.3897/mycokeys.104.112149

Phukhamsakda C, McKenzie EHC, Phillips AJL, Jones EBG, Bhat DJ, Stadler M, Bhunjun C, Wanasinghe DN, Thongbai B, Camporesi E, Ertz D, Jayawardena RS, Perera RH, Ekanayake AH, Tibpromma S, Doilom M, Xy JC, Hyde KD (2020) Microfungi associated with *Clematis* (Ranunculaceae) with an integrated approach to delimiting species boundaries. Fungal Diversity 102: 1–203. https://doi.org/10.1007/s13225-020-00448-4

Phukhamsakda C, Nilsson RH, Bhunjun CS, Gomes de Farias AR, Sun YR, Wijesinghe SN, Raza M, Bao DF, Lu L, Tibpromma S, Dong W, Tennakoon DS, Tian XG, Xiong YR, Karunarathna SC, Cai L, Luo ZL, Wang Y, Manawasinghe IS, Camporesi E, Kirk PM, Promputtha I, Kuo CH, Su HY, Doilom M, Li Y, Fu YP, Hyde KD (2022) The numbers of fungi: Contributions from traditional taxonomic studies and challenges of metabarcoding. Fungal Diversity 114: 327–386. https://doi.org/10.1007/s13225-022-00502-3

Phurbu D, Huang JE, Song S, Ni Z, Zhou X, Li S, Cai L, Liu F (2025) Diversity of culturable fungi in six Tibetan Plateau lakes, with descriptions of eight new taxa. Mycology 16(2): 670–689. https://doi.org/10.1080/21501203.2024.2333300

Rahimi-Nia Z, Mohammadi H, Sohrabi M, Voglmayr H (2025) Diversity and pathogenicity of Phaeoacremonium species infecting Haloxylon and Tamarix species in Iran. Plant Pathology 74(4): 1024–1042. https://doi.org/10.1111/ppa.14070

Rambaut A (2012) FigTree version 1.4.0. http://tree.bio.ed.ac.uk/software/ffgtree

Rannala B, Yang Z (1996) Probability distribution of molecular evolutionary trees: A new method of phylogenetic inference. Journal of Molecular Evolution 43(3): 304–311. https://doi.org/10.1007/BF02338839

Rappaz F (1995) Anthostomella and related xylariaceous fungi on hard wood from Europe and North America. Mycologia Helvetica 7: 99–168. https://doi.org/10.5169/seals-1036369

Réblová M (2011) New insights into the systematics and phylogeny of the genus *Jattaea* and similar fungi of the Calosphaeriales. Fungal Diversity 49: 167–198. https://doi.org/10.1007/s13225-011-0099-8

Réblová M, Mostert L (2007) *Romellia* is congeneric with *Togninia* and description of *Conidiotheca* gen. nov. for one species of this genus with polysporous asci. Mycological Research 111: 299–307. https://doi.org/10.1016/j.mycres.2006.12.002

Réblová M, Mostert L, Gams W, Crous PW (2004) New genera in the Calosphaeriales: *Togniniella* and its anamorph *Phaeocrella*, and *Calosphaeriophora* as anamorph of *Calosphaeria*. Studies in Mycology 50: 533–550.

Réblová M, Jaklitsch WM, Réblová K, Štěpánek V (2015) Phylogenetic reconstruction of the Calosphaeriales and Togniniales using fve genes and predicted RNA secondary structures of ITS, and *Flabellascus tenuirostris* gen. et sp. nov. PLOS ONE 10(12): e0144616. https://doi.org/10.1371/journal.pone.0144616

Rehner SA, Buckley EA (2005) Beauveria phylogeny inferred from nuclear ITS and EF1-α sequences: Evidence for cryptic diversification and links to *Cordyceps* teleomorphs. Mycologia 97: 84–98. https://doi.org/10.1080/15572536.2006.11832842

Ren GC, Wanasinghe DN, de Farias ARG, Hyde KD, Yasanthika E, Xu J, Balasuriya A, Chethana KWT, Gui H (2022a) Taxonomic novelties of woody litter fungi (Didymosphaeriaceae, Pleosporales) from the Greater Mekong Subregion. Biology (Basel) 11(11): 1660. https://doi.org/10.3390/biology11111660

Ren GC, Wanasinghe DN, Jeewon R, Monkai J, Mortimer PE, Hyde KD, Xu JC, Gui H (2022b) Taxonomy and phylogeny of the novel rhytidhysteron-like collections in the Greater Mekong Subregion. MycoKeys 86: 65–85. https://doi.org/10.3897/mycokeys.86.70668

Ren GC, Jayasiri SC, Tibpromma S, De Farias ARG, Chethana KWT, Faraj KH, Wanasinghe DN, Xu JC, Hyde KD, Gui H (2024) Saprobic ascomycetes associated with woody litter from the Greater Mekong Subregion (Southwestern China and Northern Thailand). Mycosphere: Journal of Fungal Biology 15(1): 954–1082. https://doi.org/10.5943/mycosphere/15/1/8

Ronquist F, Huelsenbeck JP (2003) MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics (Oxford, England) 19(12): 1572–1574. https://doi.org/10.1093/bioinformatics/btg180

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: Efffcient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61(3): 539–542. https://doi.org/10.1093/sysbio/sys029

Saccardo PA, Sydow P (1902) Sylloge Fungorum 16: 421. https://www.cybertruffle.org.uk/cyberliber/02971/0421.htm

Samaradiwakara NP, deFarias ARG, Tennakoon DS, Aluthmuhandiram JVS, Bhunjun CS, Chethana KWT, Kumla J, Lumyong S (2023) Appendage-bearing Sordariomycetes from Dipterocarpusalatus Leaf Litter in Thailand. Journal of Fungi (Basel, Switzerland) 9: 625. https://doi.org/10.3390/jof9060625

Samarakoon MC, Thongbai B, Hyde KD, Brönstrup M, Beutling U, Lambert C, Miller AN, Liu JK, Promputtha I, Stadler M (2020) Elucidation of the life cycle of the endophytic genus *Muscodor* and its transfer to Induratia in Induratiaceae fam. nov., based on a polyphasic taxonomic approach. Fungal Diversity 101: 177–210. https://doi.org/10.1007/s13225-020-00443-9

Samarakoon MC, Hyde KD, Maharachchikumbura SSN, Stadler M, Jones EBG, Promputtha I, Suwannarach N, Camporesi E, Bulgakov TS, Liu JK (2022) Taxonomy, phylogeny, molecular dating and ancestral state reconstruction of Xylariomycetidae (Sordariomycetes). Fungal Diversity 112(1): 1–88. https://doi.org/10.21203/rs.3.rs-935829/v1

Samarakoon MC, Lumyong S, Manawasinghe IS, Suwannarach N, Cheewangkoon R (2023) Addition of Five Novel Fungal Flora to the Xylariomycetidae (Sordariomycetes, Ascomycota) in Northern Thailand. Journal of Fungi (Basel, Switzerland) 9: 1065. https://doi.org/10.3390/jof9111065

Senanayake IC, Rathnayaka AR, Marasinghe DS, Calabon MS, Gentekaki E, Lee HB, Hurdeal VG, Pem D, Dissanayake LS, Wijesinghe SN, Bundhun D, Nguyen TT, Goonasekara ID, Abeywickrama PD, Bhunjun CS, Jayawardena RS, Wanasinghe DN, Jeewon R, Bhat DJ, Xiang MM (2020) Morphological approaches in studying fungi: Collection, examination, isolation, sporulation and preservation. Mycosphere: Journal of Fungal Biology 11(1): 2678–2754. https://doi.org/10.5943/mycosphere/11/1/20

Senwanna C, Phookamsak R, Bahkali AH, Elgorban AM, Cheewangkoon R, Hyde KD (2018) *Neolinocarpon phayaoense* sp. nov.(Linocarpaceae) from Thailand. Phytotaxa 362(1): 77–86. https://doi.org/10.11646/phytotaxa.362.1.6

Shen HW, Bao DF, Luan S, Wanasinghe DN, Du TY, Hongsanan S, Yang J, Zhang JY, Tang X, Bhatt JD, Xu RJ, Wang WP, Su XJ, Li YX, Zhao Q, Liu JK, Lu YZ, Luo ZL, Yang LQ (2025) Taxonomy and phylogeny of lignicolous freshwater fungi from plateau lakes in Yunnan Province, China. Fungal Diversity 134: 635–899. https://doi.org/10.1007/s13225-025-00564-z

Stamatakis A (2014) RAxML Version 8: A tool for Phylogenetic Analysis and Post-Analysis of Large Phylogenies. Bioinformatics (Oxford, England) 30(9): 1312–1313. https://doi.org/10.1093/bioinformatics/btu033

Sugita R, Tanaka K (2022) *Thyridium* revised: Synonymisation of *Phialemoniopsis* under *Thyridium* and establishment of a new order, Thyridiales. MycoKeys 86: 147–176. https://doi.org/10.3897/mycokeys.86.78989

Sułkowska-Ziaja K, Trepa M, Olechowska-Jarząb A, Nowak P, Ziaja M, Kała K, Muszyńska B (2023) Natural compounds of fungal origin with antimicrobial activity—Potential cosmetics applications. Pharmaceuticals 16(9): 1200. https://doi.org/10.3390/ph16091200

Sun JE, Fu L, Norphanphoun C, Chen XJ, Yu LF, Hyde KD, McKenzie EHC, Wang Y, Yang ZF, Liu FQ (2024) Study on the diversity of rust pathogens from different hosts in Guizhou Province, China. Mycosphere: Journal of Fungal Biology 15(1): 473–653. https://doi.org/10.5943/mycosphere/15/1/4

Thiyagaraja V, Hyde KD, Piepenbring M, Davydov EA, Dai DQ, Abdollahzadeh J, Bundhun D, Chethana KWT, Crous PW, Gajanyake AJ, Gomdola D, Haelewaters D, Johnston PR, Mardones M, Perera RH, Senanayake IC, Tibpromma S, Yasanthika WAE, Abbasi MW, Abdel-Wahab MA, Absalan S, Acharya K, Afshari N, Aouali S, Aptroot A, Armand A, Avasthi S, Bao DF, Bhat DJ, Blondelle A, Boonmee S, Boonyuen N, Braun U, Čadež N, Calabon MS, Cazabonne J, Chakraborty N, Cheewangkoon R, Chen K-H, Coleine C, Darmostuk V, Daroodi Z, Dasgupta D, de Groot MD, de Hoog S, Deng W, Dissanayake AJ, Dissanayake LS, Doilom M, Dong W, Ertz D, Fortuna JL, Gautam AK, Gorczak M, Groenewald M, Groenewald JZ, Gunaratne A, Han Y, Hongsanan S, Hou CL, Htet YM, Huang Q, Huang SK, Huanraluek N, Jayalal RGU, Jayasiri SC, Jayawardena RS, Jiang SH, Jones EBG, Karimi O, Karunarathna SC, Khuna S, Kossmann T, Kularathnage ND, Lestari AS, Li CJY, Li JF, Lin CG, Liu JK, Liu Y, Lu L, Lu YZ, Luo ZL, Ma J, Madagammana AS, Maharachchikumara SSN, Marasinghe DS, Martzoukou E, Marin-Felix Y, Miller AN, Monkai J, Noorabadi MT, Norphanphoun C, Olariaga I, Opina LAD, Pang KL, Peng X, Péter G, Phillips AJL, Pineda MM, Prieto M, Quan Y, Quandt A, Rajeshkumar KC, Rambold G, Raymundo T, Raza M, Réblová M, Samaradiwakara NP, Sandoval-Denis M, Sarma VV, Schuster TM, Seifollah E, Selbmann L, Su H, Sun YR, Tehler A, Tennakoon DS, Thambugala KM, Tian WH, Tsurykau A, Valenzuela R, Verma S, Wang JZ, Wang WP, Wang XY, Wang Y, Wang YL, Wang Y, Wei DP, Wen T, Wijesinghe D, Wimalasena MK, Worthy FR, Wu HX, Xu L, Yakovchenko LS, Yan J, Zeng XY, Zhang SN, Zhang ZY, Zhao Q, Wanasinghe DN (2025) Orders of Ascomycota. Mycosphere: Journal of Fungal Biology 16(1): 536–1411. https://doi.org/10.5943/mycosphere/16/1/8

Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG (1997) The ClustalX windows interface: Flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Research 24(24): 4876–4882. https://doi.org/10.1093/nar/25.24.4876

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. Journal of Bacteriology 172: 4238–4246. https://doi.org/10.1128/jb.172.8.4238-4246.1990

Vitoria NS, Cavalcanti MA, dos Santos CD, Pereira J, Bezerra JL (2013) *Neolinocarpon attaleae* sp. nov. on *Attalea funifera* (Arecaceae) from Brazil. Mycotaxon 123: 141–145. https://doi.org/10.5248/123.141

Voglmayr H, Friebes G, Gardiennet A, Jaklitsch WM (2018) *Barrmaelia* and *Entosordaria* in Barrmaeliaceae (fam. nov., Xylariales) and critical notes on *Anthostomella*-like genera based on multigene phylogenies. Mycological Progress 17: 155–177. https://doi.org/10.1007/s11557-017-1329-6

Wanasinghe DN, Maharachchikumbura SSN (2023) Exploring the diversity and systematics of Phaeosphaeriaceae: Taxonomic novelties from ecologically diverse habitats and their phylogenetic resolution. Journal of Fungi (Basel, Switzerland) 9(8): 853. https://doi.org/10.3390/jof9080853

Wanasinghe DN, Mortimer PE, Xu JC (2021) Insight into the systematics of microfungi colonizing dead woody twigs of *Dodonaea viscosa* in Honghe (China). Journal of Fungi (Basel, Switzerland) 7(3): 180. https://doi.org/10.3390/jof7030180

Wanasinghe DN, Nimalrathna TS, Qin Xian L, Faraj TK, Xu J, Mortimer PE (2024) Taxonomic novelties and global biogeography of *Montagnula* (Ascomycota, Didymosphaeriaceae). MycoKeys 101: 191–232. https://doi.org/10.3897/mycokeys.101.113259

Wanasinghe DN, Phookamsak R, Dissanayake LS, Xu J (2025) Unexplored microfungal diversity from dead woody litter in the dry-hot valleys of Honghe (Yunnan, China). Studies in Fungi 10: e017. https://doi.org/10.48130/sif-0025-0016

Wang K, Cai L (2023) Overview of the historical and current status of fungal taxonomy and diversity in China. Mycosystema 42(1): 50–62. https://doi.org/10.13346/j.mycosystema.220497

Wang HY, Li X, Dong CB, Zhang YW, Chen WH, Liang JD, Han YF (2024) Two new species of Sordariomycetes (Chaetomiaceae and Nectriaceae) from China. MycoKeys 102: 301–315. https://doi.org/10.3897/mycokeys.102.114480

White TJ, Bruns T, Lee S, Taylor JW (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR protocols: A guide to methods and applications. Academic Press San Diego, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wijayawardene NN, Hyde KD, Lumbsch HT, Liu JK, Maharachchikumbura SSN, Ekanayaka AH, Tian Q, Phookamsak R (2018) Outline of ascomycota: 2017. Fungal Diversity 88: 167–263. https://doi.org/10.1007/s13225-018-0394-8

Wijayawardene NN, Hyde KD, Dai DQ, Sánchez-García M, Goto BT, Saxena RK, Erdoğdu M, Selçuk F, Rajeshkumar KC, Aptroot A, Błaszkowski J, Boonyuen N, da Silva GA, de Souza FA, Dong W, Ertz D, Haelewaters D, Jones EBG, Karunarathna SC, Kirk PM, Kukwa M, Kumla J, Leontyev DV, Lumbsch HT, Maharachchikumbura SSN, Marguno F, Martínez-Rodríguez P, Mešić A, Monteiro JS, Oehl F, Pawłowska J, Pem D, Pfliegler WP, Phillips AJL, Pošta A, He MQ, Li JX, Raza M, Sruthi OP, Suetrong S, Suwannarach N, Tedersoo L, Thiyagaraja V, Tibpromma S, Tkalčec Z, Tokarev YS, Wanasinghe DN, Wijesundara DSA, Wimalaseana SDMK, Madrid H, Zhang GQ, Gao Y, Sánchez-Castro I, Tang LZ, Stadler M, Yurkov A, Thines M (2022) Outline of Fungi and fungus-like taxa – 2021. Mycosphere: Journal of Fungal Biology 13(1): 53–453. https://doi.org/10.5943/mycosphere/13/1/2

Xu XL, Yang CL, Jeewon R, Wanasinghe DN, Liu XL, Xiao QG (2020) Morpho-molecular diversity of Linocarpaceae (Chaetosphaeriales): *Claviformispora* gen. nov. from decaying branches of Phyllostachys heteroclada. MycoKeys 69(4): 113–129. https://doi.org/10.3897/mycokeys.69.54231

Yang J, Liu LL, Jones EBG, Hyde KD, Liu ZY, Bao DF, Liu NG, Li WL, Shen HW, Yu XD, Liu JK (2023) Freshwater fungi from karst landscapes in China and Thailand. Fungal Diversity 119(1): 1–212. https://doi.org/10.1007/s13225-023-00514-7

Yu XD, Zhang SN, Liu JK (2022) Morpho-phylogenetic evidence reveals novel Pleosporalean taxa from Sichuan Province, China. Journal of Fungi (Basel, Switzerland) 8(7): 720. https://doi.org/10.3390/jof8070720

Yue JZ, Eriksson OE (1987) *Sinosphaeria bambusicola* gen. et sp. nov., (Thyridiaceae fam. nov.). Systema Ascomycetum 6: 229–236.

Zhang ZF, Zhou SY, Eurwilaichitr L, Ingsriswang S, Raza M, Chen Q, Zhao P, Liu F, Cai L (2021) Culturable mycobiota from Karst caves in China II, with descriptions of 33 new species. Fungal Diversity 106: 29–136. https://doi.org/10.1007/s13225-020-00453-7

Zhang X, Dai DQ, Du TY, Karunarathna SC, Tibpromma S (2023a) Morpho-phylogeny characterization of *Linocarpon bambusina* sp. nov. (Linocarpaceae, Chaetosphaeriales) associated with bamboo in Yunnan Province, China. Phytotaxa 584(2): 89–103. https://doi.org/10.5281/zenodo.7646433

Zhang JF, Liu JK, Hyde KD, Chen YY, Ran HY, Liu ZY (2023b) Ascomycetes from karst landscapes of Guizhou Province, China. Fungal Diversity 122(1): 1–160. https://doi.org/10.1007/s13225-023-00524-5

Zhang X, Dai D, Du T, Karunarathna SC, Tibpromma S (2023c) Morpho-phylogeny characterization of *Linocarpon bambusina* sp. nov. (Linocarpaceae, Chaetosphaeriales) associated with bamboo in Yunnan Province, China. Phytotaxa 584(2): 89–103. https://doi.org/10.11646/phytotaxa.584.2.2

Zhang SN, Hyde KD, Jones EBG, Yu XD, Cheewangkoon R, Liu JK (2024) Current insights into palm fungi with emphasis on taxonomy and phylogeny. Fungal Diversity 127(1): 55–301. https://doi.org/10.1007/s13225-024-00536-9

Zhang X, Tibpromma S, Karunarathna SC, Du TY, Han LS, Elgorban AM, Kumla J, Senwanna C, Dai DQ, Suwannarach N, Wang HH (2025) Additions to the saprobic fungi (Ascomycota) associated with macadamia trees from the Greater Mekong Subregion. MycoKeys 113: 1–29. https://doi.org/10.3897/mycokeys.113.140031